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TECH CENTER 1600/2900

TRFP CHAIN 1, LEADER A

10	20	30	40	50	60
CTGCATCATGAAGGGGGCTCGTGTCTCGTGCCTCTGGCTGCCTTGCTCTGATCTG <u>C I M K G A R V L V L L W A A A L L L I W</u>					
70	80	90	100	110	120
GGGTGGAAATTGTGAAATTGCCAGCCGTGAAGAGGGATGTTGACCTATTCCCTGACGGG <u>G G N C E I C P A V K R D V D L F L T G</u>					
130	140	150	160	170	180
AACCCCCGACGPATATGTTGAGCAAGTGGCACAAATACAAAGCACTACCTGTAGTATTGGA <u>T P D E Y V E Q V A Q Y K A L P V V L E</u>					
190	200	210	220	230	240
AAATGCCAGAAATACTGAAGAACTGCCGTTGATGCAAAATGACAGAAGAGGATAAGGAGAA <u>N A R I L K N C V D A K M T E E D K E N</u>					
250	260	270	280	290	300
TGCTCTCAGCTTGCTGGACAAAATATACACAAAGTCCTCTGTGTTAAAGGAGCCATCACTG <u>A L S L L D K I Y T S P L C -</u>					
310	320	330	340	350	360
CCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTGCCATGT <u>CCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTGGCAATTCAAACAAAAAAA</u>					
370	380	390	400	410	

Fig. 1



TRFP CHAIN 1, LEADER B

10	20	30	40	50	60
GGCCTGGCGGTGCTCCTGGAAAAGGATGTTAGACGCAGCCCTCCCACCCCTGCCCTACTGTT					
A	W	R	C	S	W
70	80	90	100	110	120
TGCGGCCACAGCAGATTGTGAAATTTGCCAGCCGTGAAGAGGGATGTTGACCTATTCTT					
A	A	T	A	D	C
130	140	150	160	170	180
GACGGGAACCCCCGACGAATATGTTGAGCAAGTGGCACAAATACAAAGCACTACCTGTAGT					
T	G	T	P	D	E
190	200	210	220	230	240
ATTGGAAAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAA					
L	E	N	A	R	I
250	260	270	280	290	300
GGAGAAATGCTCTCAGTTGCTGGACAAAATATACACAAAGTCCTCTGTGTTAAAGGAGCCA					
E	N	A	L	S	L
310	320	330	340	350	360
TCACTGCCAGGAGCCCTAACCGAACACTGAAGTACTGATCACTAACGTAGTCTCAGCAGCCTG					
370	380	390	400	410	420
CCATGTCCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTTGCAATTCAAACAAA					

Fig. 2



TRFP CHAIN 2, LONG FORM

10	20	30	40	50	60
TGACACGATGAGGGGGCACTGCTTGTGCTGGCATTGCTGGTACCCAAGCGCTGGCGT D T M R G A L L V L A L L V T Q A L G V					
70	80	90	100	110	120
CAAGATGGCGGAAACTTGCCTTATTTTATGACGTCTTTGCAGGTGGCCAATGGAAA K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
TGAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAAGAGAGAACAGC E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
CATGAAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTGGATGG M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
ACTAGTCATGACAACCATCAGCTCCAGCAAAGATTGCATGGGTGAAGCAGTTCAGAACAC L V M T T I S S S K D C M G E A V Q N T					
310	320	330	340	350	360
CGTAGAAGATCTCAAGCTGAACACTTGGGGAGATGAATCTTGCCACTGATGCCCTTC V E D L K L N T L G R -					
370	380	390	400	410	420
TGAGCCCCATCCTCCTGCCCTGTTCTTACACCTAAAGCTGGAATCCAGACACCTGTCCT					
430	440	450	460	470	
CACCTAATTCACTCTCAATCAGGCTGACTAGAATAAAATAACTGCATCTTAAAAAA					

Fig. 3



TRFP1 CHAIN 2, SHORT FORM

10	20	30	40	50	60
<pre> GACACGATGAGGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAAGCGCTGGCGTC D T M R G A L L V L A L L V T Q A L G V </pre>					
70	80	90	100	110	120
<pre> AAGATGGCGGAGACGTGCCCATTTTATGACGTCTTTGCGGTGCCAATGGAAAT K M A E T C P I F Y D V F F A V A N G N </pre>					
130	140	150	160	170	180
<pre> GAATTACTGTTGGACTTGTCCCTCACAAAGTCATGCTACTGAACCAGAGAGAACAGCC E L L L D L S L T K V N A T E P E R V A </pre>					
190	200	210	220	230	240
<pre> ATGAAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGCTTGGATGGA M K K I Q D C Y V E N G L I S R V L D G </pre>					
250	260	270	280	290	300
<pre> CTAGTCATGATAGCCATCAACGAATATTGATGGGTGAAGCAGTTCAGAACACCGTAGAA L V M I A I N E Y C M G E A V Q N T V E </pre>					
310	320	330	340	350	360
<pre> GATCTCAAGCTGAACACTTGGGAGATGAATCTTGCCACTGATGCCCTTGAGCCC D L K L N T L G R - </pre>					
370	380	390	400	410	420
<pre> CATCCTCCTGTCTGTTTACACCTAAAGCTGGAATCCAGACACCTGCTCACCTAA </pre>					
430	440	450	460		
<pre> TTCACTCTCAATCAGGCTGACTAGAATAAAATACTGCATCTTAAAAAA </pre>					

Fig. 4



TRFP CHAIN 2, TRUNCATED SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCAC TGCTTGTGCTGGCATTGCTGGTGACCCAAGCCGCTGGCGTC D T M R G A L L V L A L L V T O A L G V					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTATGACGTCTTTTGCGGGTGGCCAATGGAAAT K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAAGAGAGAACAGCC E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
ATGAAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTGGATGGA M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGCCATCAACGAATATTGCATGGGTGAAGCAGTTCAGAACACCGTAGAACAGATC L V M P S T N I A W V K Q F R T P -					
310	320	330	340	350	360
TCAAGCTGAACACTTGGGGAGATGAATCTTGCCACTGATGCCCTCTGAGCCCCATC					
370	380	390	400	410	420
CTCCTGTCCTGTTCTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAACCTAATTCA					
430	440	450	460		
CTCTCAATCAGGCTGACTAGAATAAAATACTGCATCTTAAAAAA					

Fig. 5



TRFP CHAIN #1 PROTEIN SEQUENCE

	-20					-10					
C1	Leader A	C I M R G A R V L V V L W A A L L L I W G G N C									
C1	Leader B	A W R C S W K R M L D A A L P P C P T B A A T A D C									
		5	10	15	20	25	30	35			
C1		E I C P A V K R D V D L F L T G T P D E Y V E Q V A Q Y K A L P V V L									
PRO.		- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
		40	45	50	55	60	65	70			
C1		E N A R I L K N C V D A K M T E D K E N A L S L L D K I Y T S P L C									
PRO.		- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	

Fig. 6



## TRFP CHAIN #2 PROTEIN SEQUENCES

C2 Leader D T M R G A L L V L A L L V T Q A L G  
C2L V R M A E T C P I F Y D V F F A V A N G N E L L D S L T R V N A T E P E R T  
C2S - - - - -  
C2ST - - - - -  
PRO. - - - - -

Fig. 7A



	45	50	55	60	65	70	75	80
C2L	AMKKIODCYYENGЛИSRVLDGLVMTTISSSKDCMGEAVQN							
C2S						IA - NE * Y - - - - -		
C2ST						P S T N I A W V K Q F R T P		
PRO.						T T - S S ( K ) - - - - -		
						IA - NE ( K ) - - - - -		
					85	90		
C2L	TVEDLKLNTRGR							
C2S						- - - - -		
PRO.	TV	-						
	AM	-						

Fig. 7B



PATIENT # 131.2 2° (TRFP:1°)

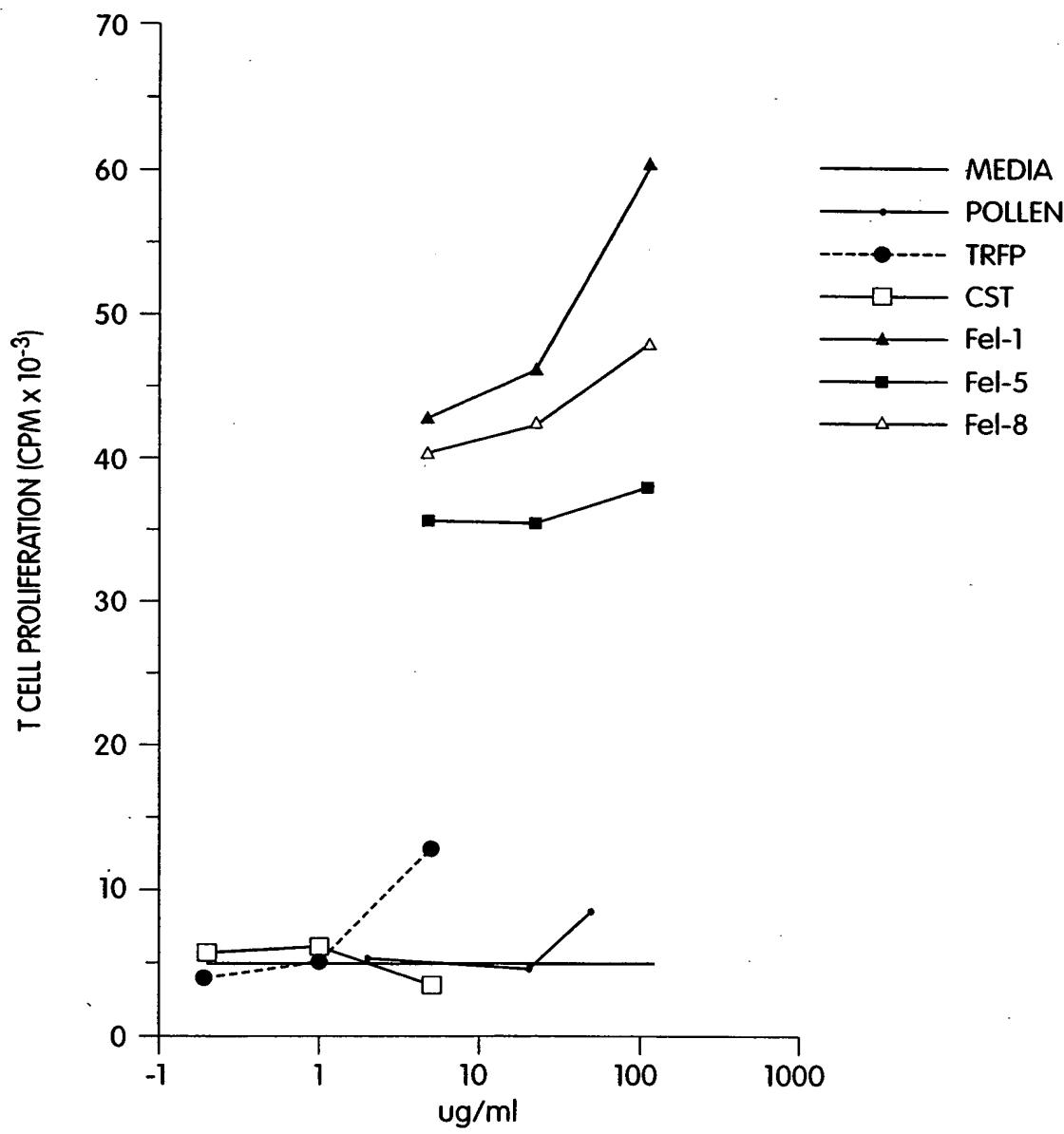


Fig. 8

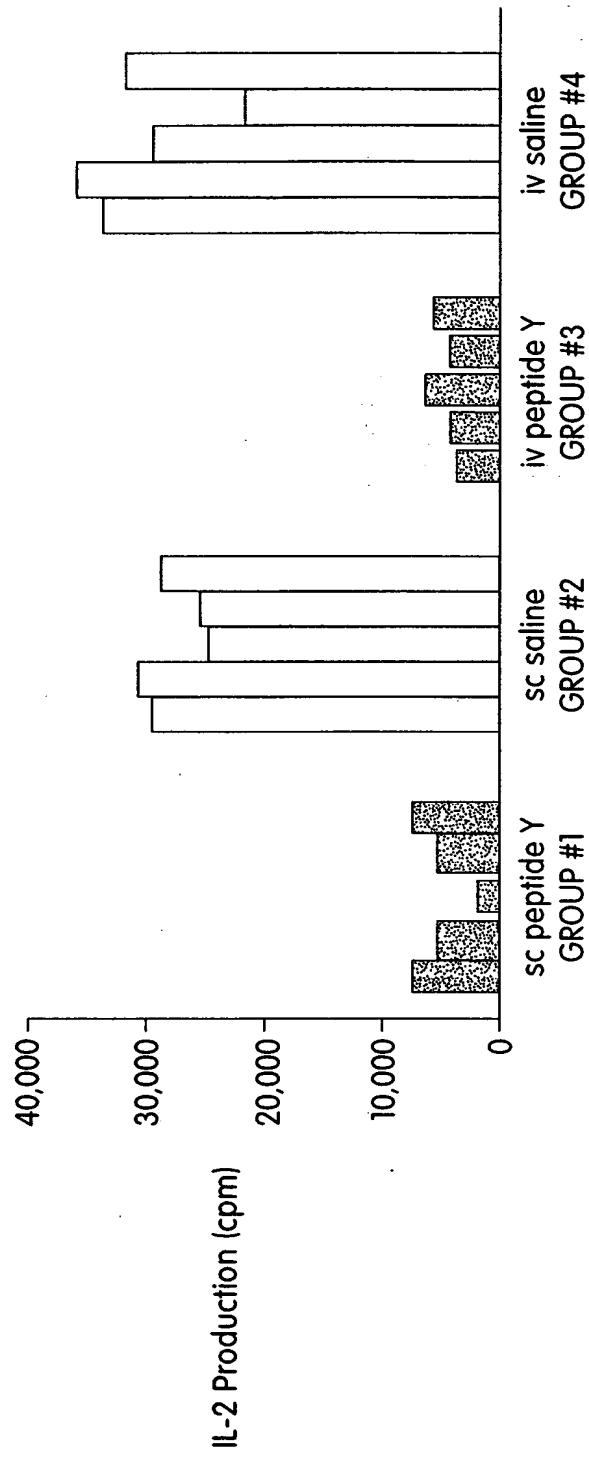
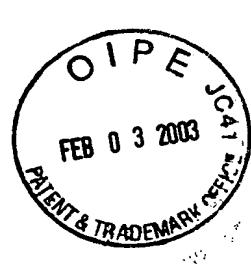


Fig. 9

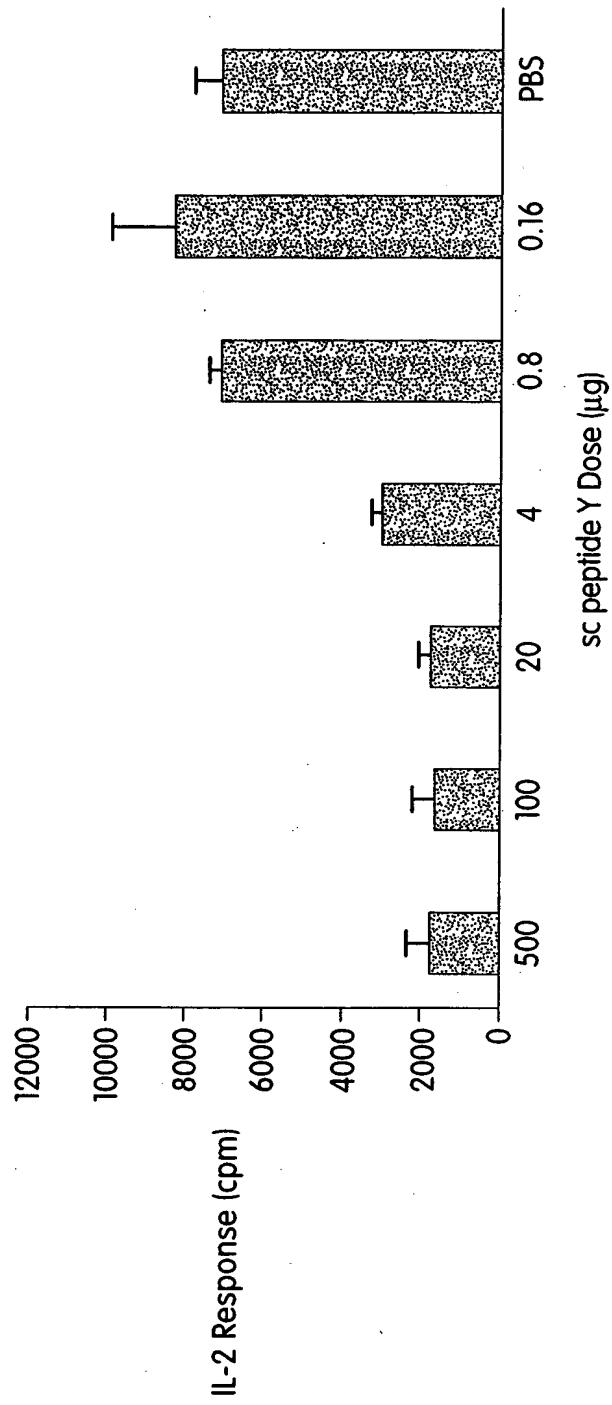


Fig. 10

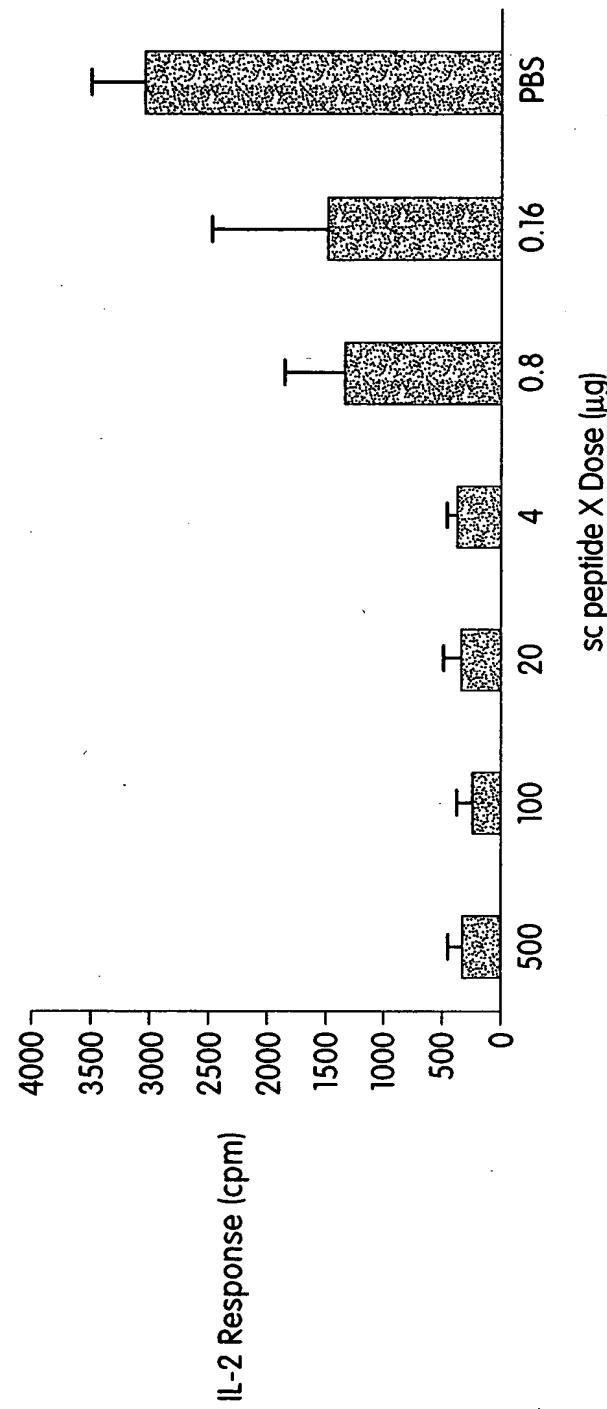


Fig. 11

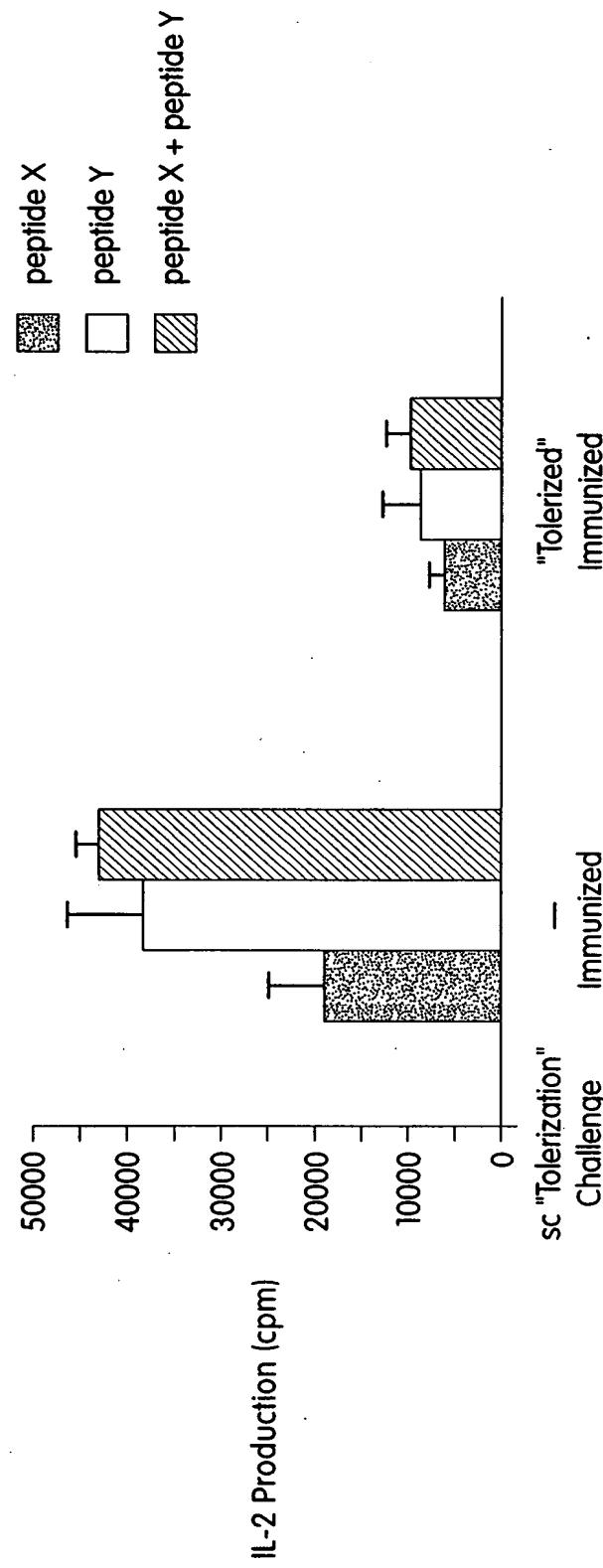


Fig. 12

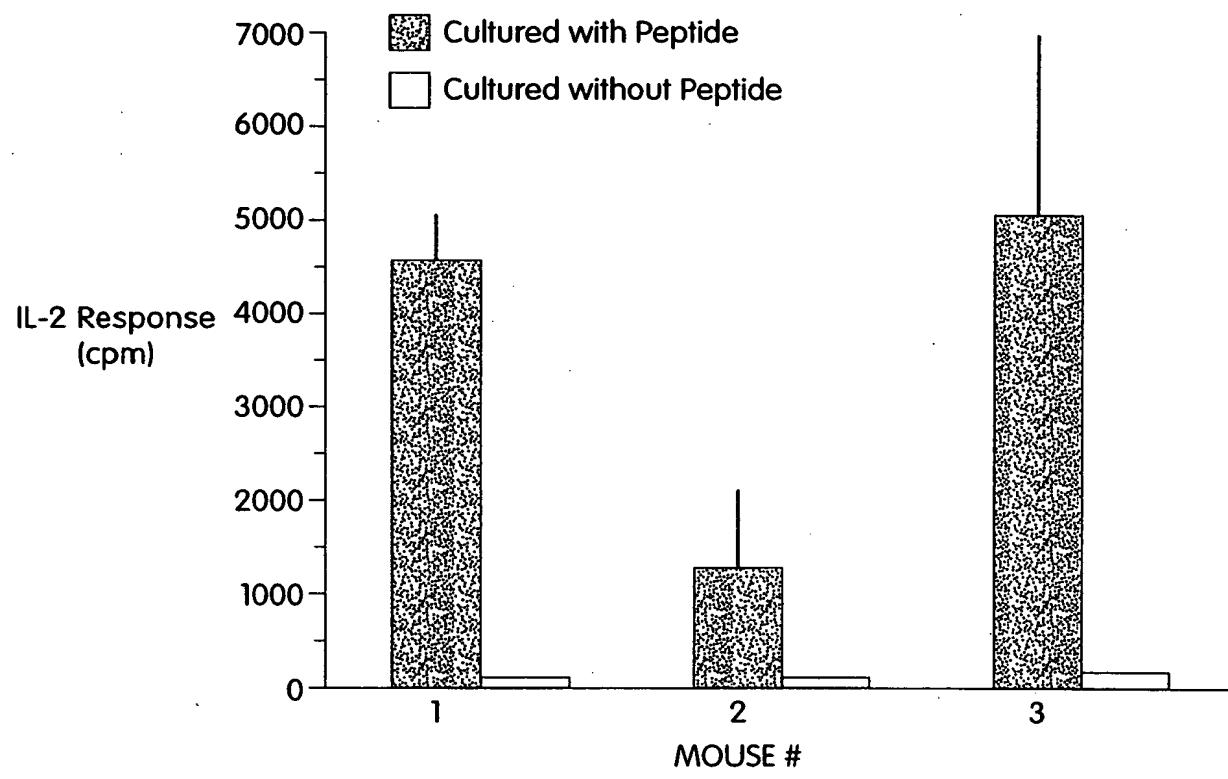


Fig. 13

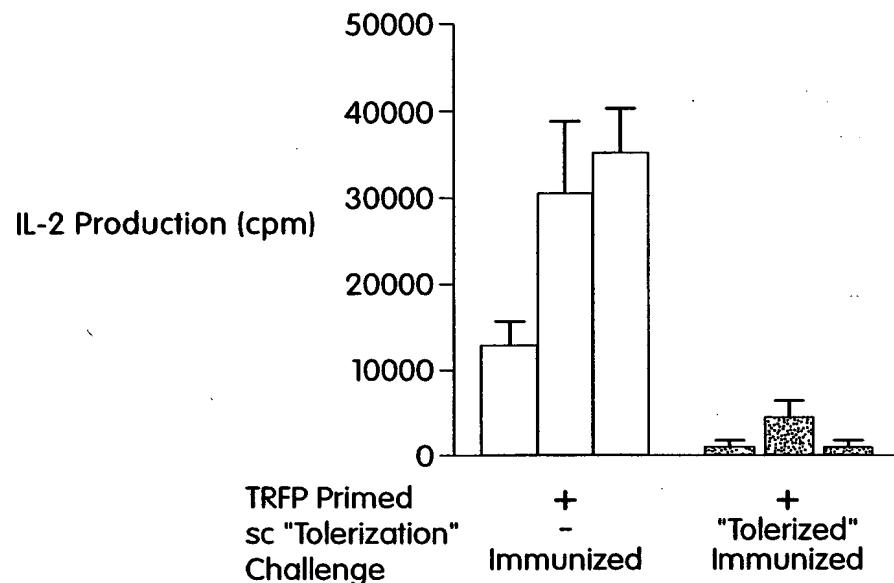


Fig. 14A

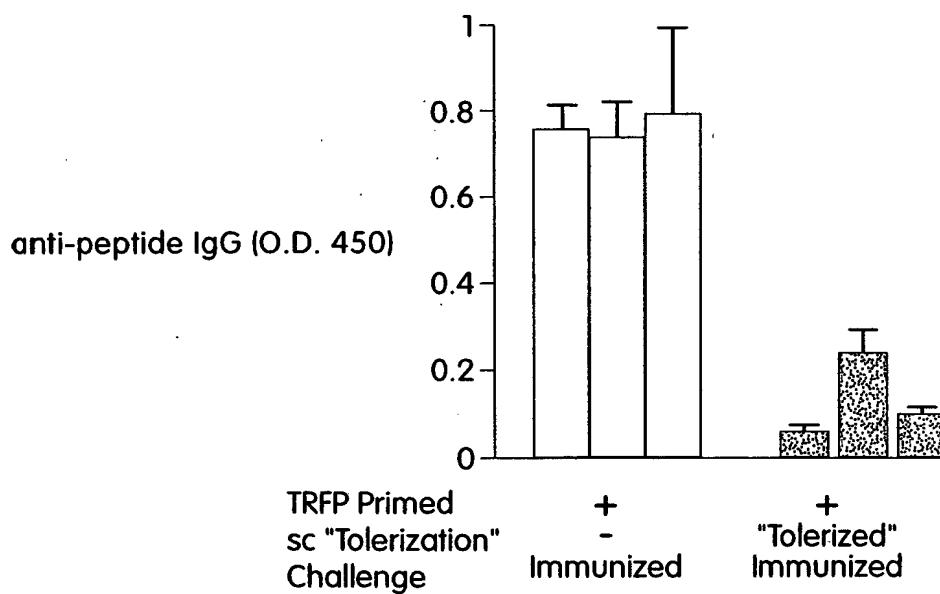


Fig. 14B

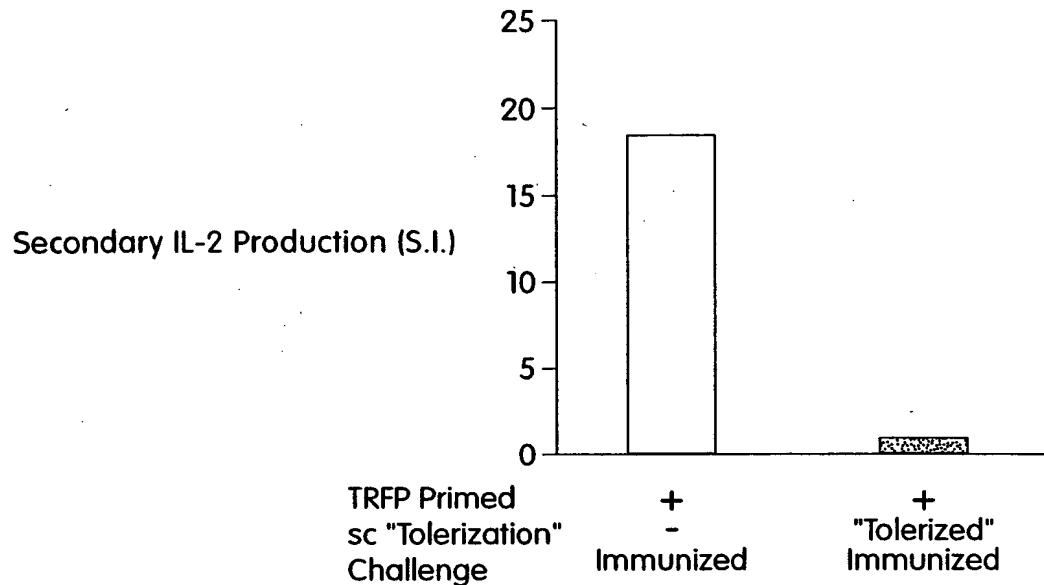


Fig. 15A

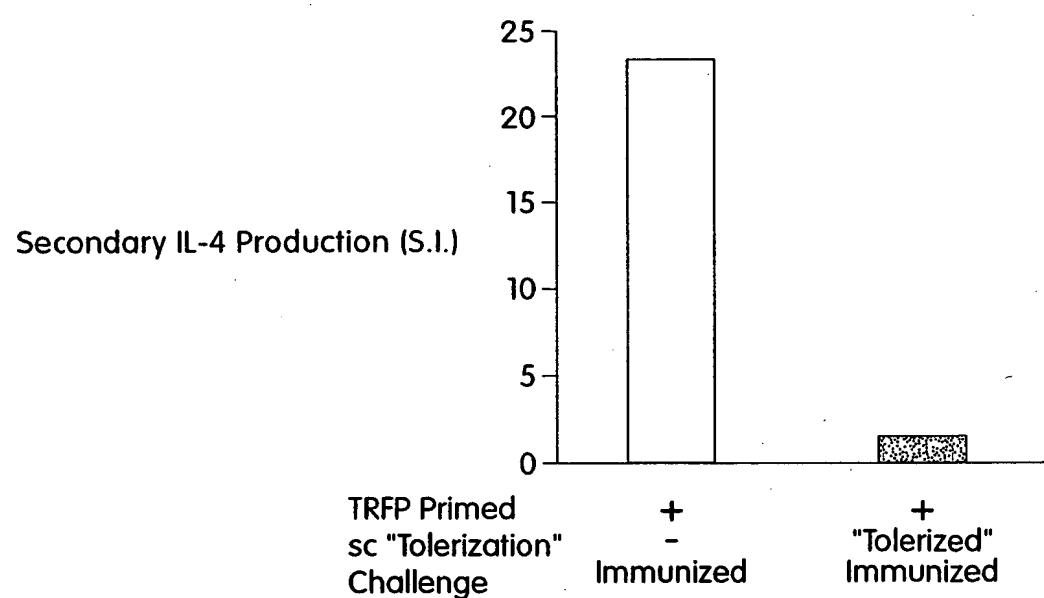


Fig. 15B

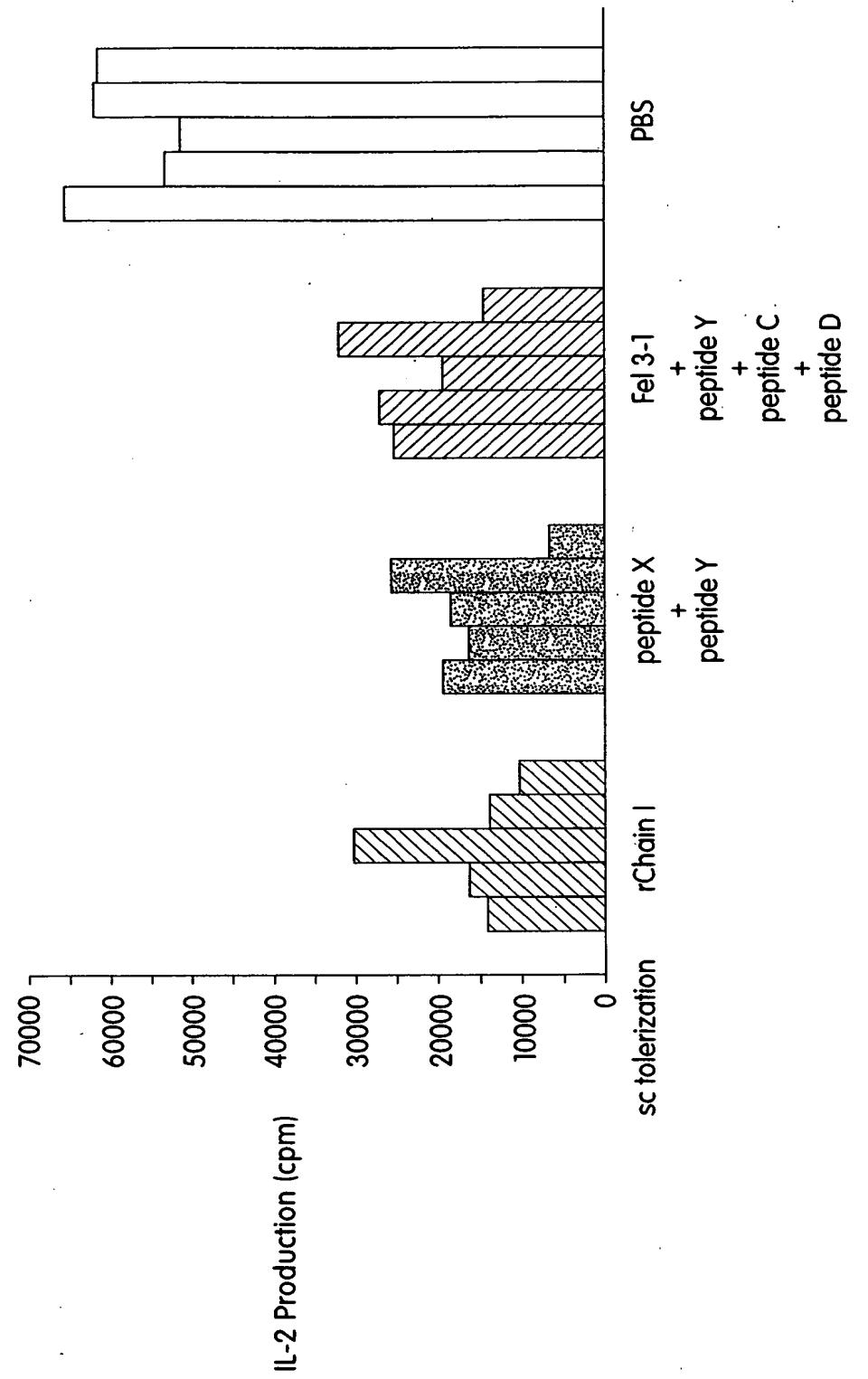


Fig. 16



SEQUENCE

PEPTIDE  
NAME

- X KRDVDLFLTGTGTPDEYVEQVAQYKALPV**
- Y KALPVVLENARILKNCVDAKMTEEDKE**
- Z FFAVANGNELLLDLSSLTKVNATEPER**
- A EEDKENALSLLDKIYTSPL**
- B MGEAVQNTVEDLKLNTLGR**
- C EEDKENALSLLDKIYT**
- D NALSLLDKIYTSPL**

Fig. 17



<b>Fel 32</b>	<b>VKMAETCPIFYDVFFAVA</b>
<b>Fel 33</b>	<b>FYDVFFAVANGNELLLD</b>
<b>Fel 34</b>	<b>NGNELLLDLSLTKVNATE</b>
<b>Fel 35</b>	<b>SLTKVNATEPERTAMKKI</b>
<b>Fel 36</b>	<b>ERTAMKKIQDCYVENGL</b>
<b>Fel 37</b>	<b>QDCYVENGLISRVLGGLV</b>
<b>Fel 38</b>	<b>ISRVLGGLVMTTISSLKDCM</b>
<b>Fel 38-1</b>	<b>ISRVLGGLVMIAINE**DCM</b>
<b>Fel 39</b>	<b>MTTISSLKDCMGEAVQNTTEVELDKLNTLGF</b>
<b>Fel 39.1</b>	<b>MIAINE**DCMGEAVQNTTEVELDKLNTLGF</b>

**Fig. 18**

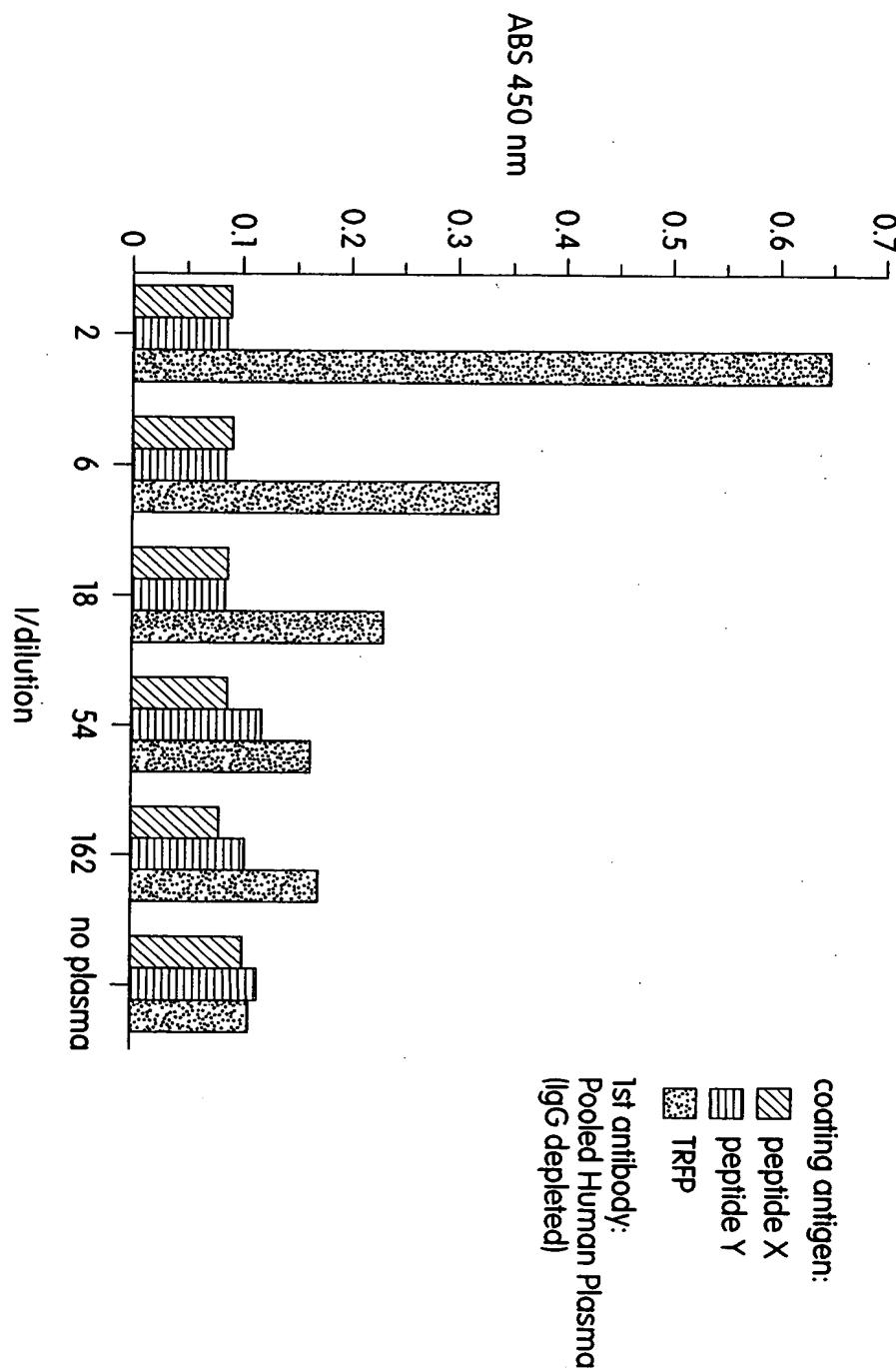


Fig. 19

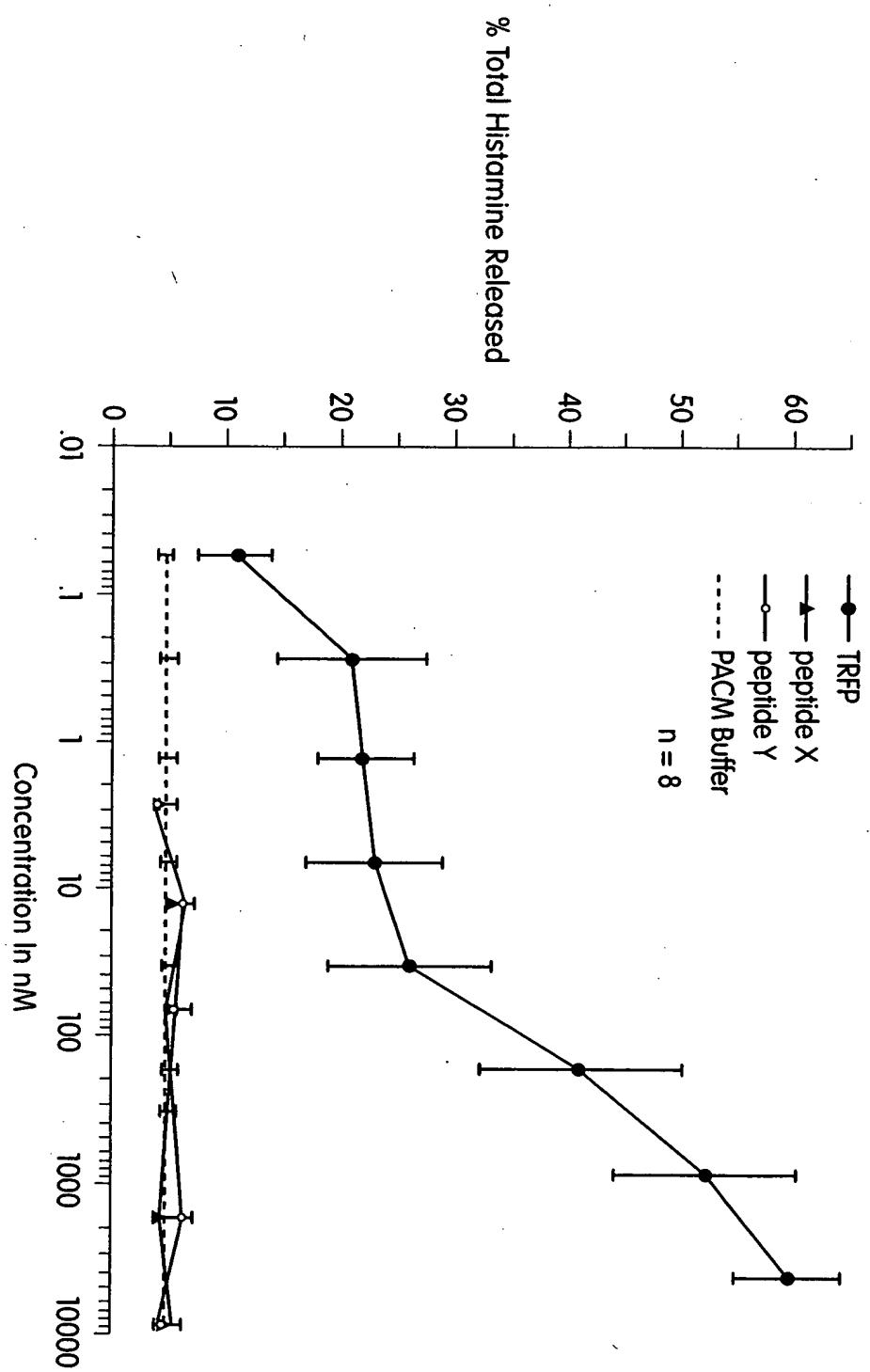


Fig. 20

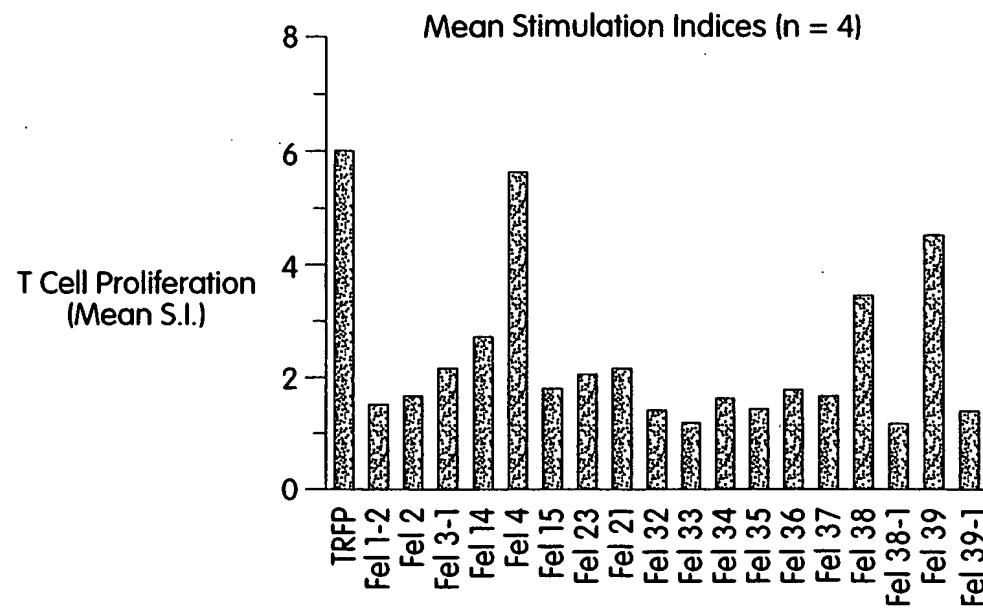


Fig. 21A

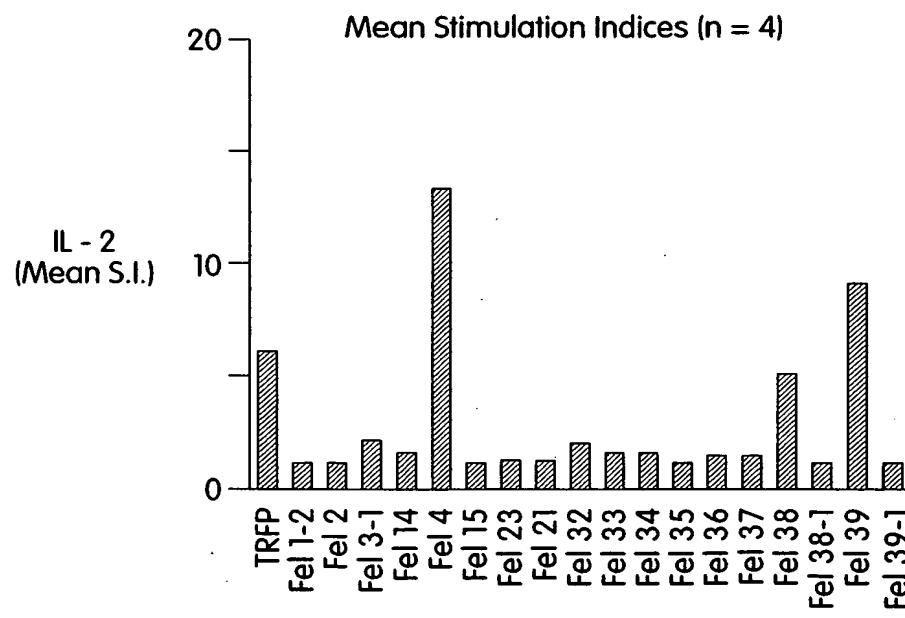


Fig. 21B

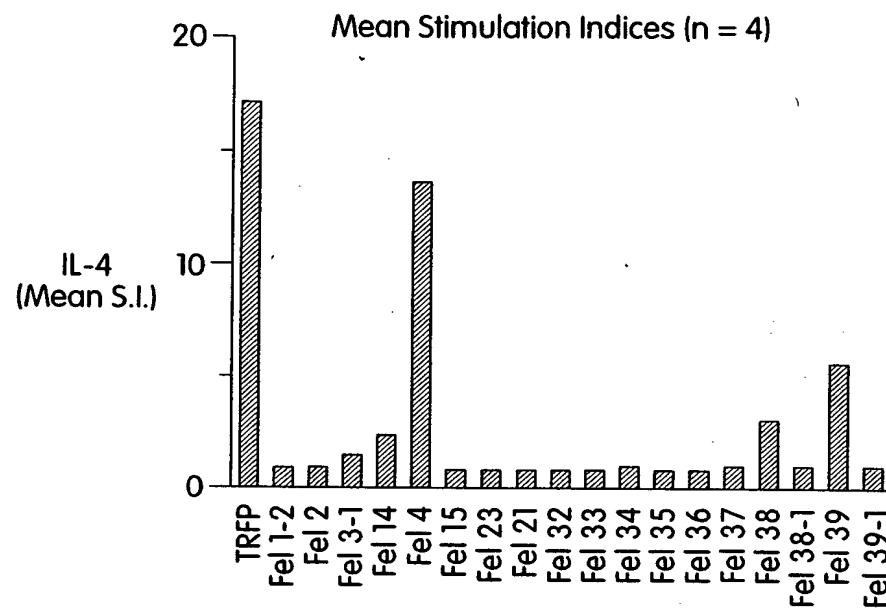


Fig. 21C

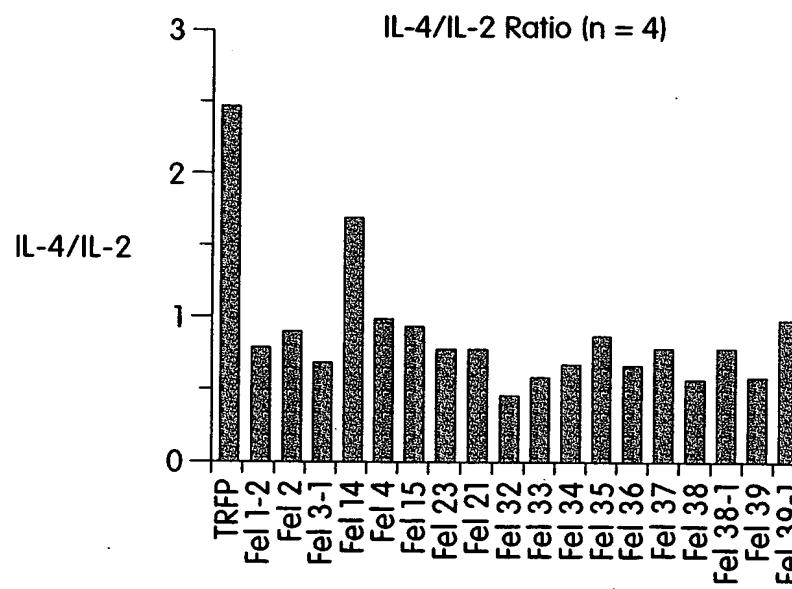
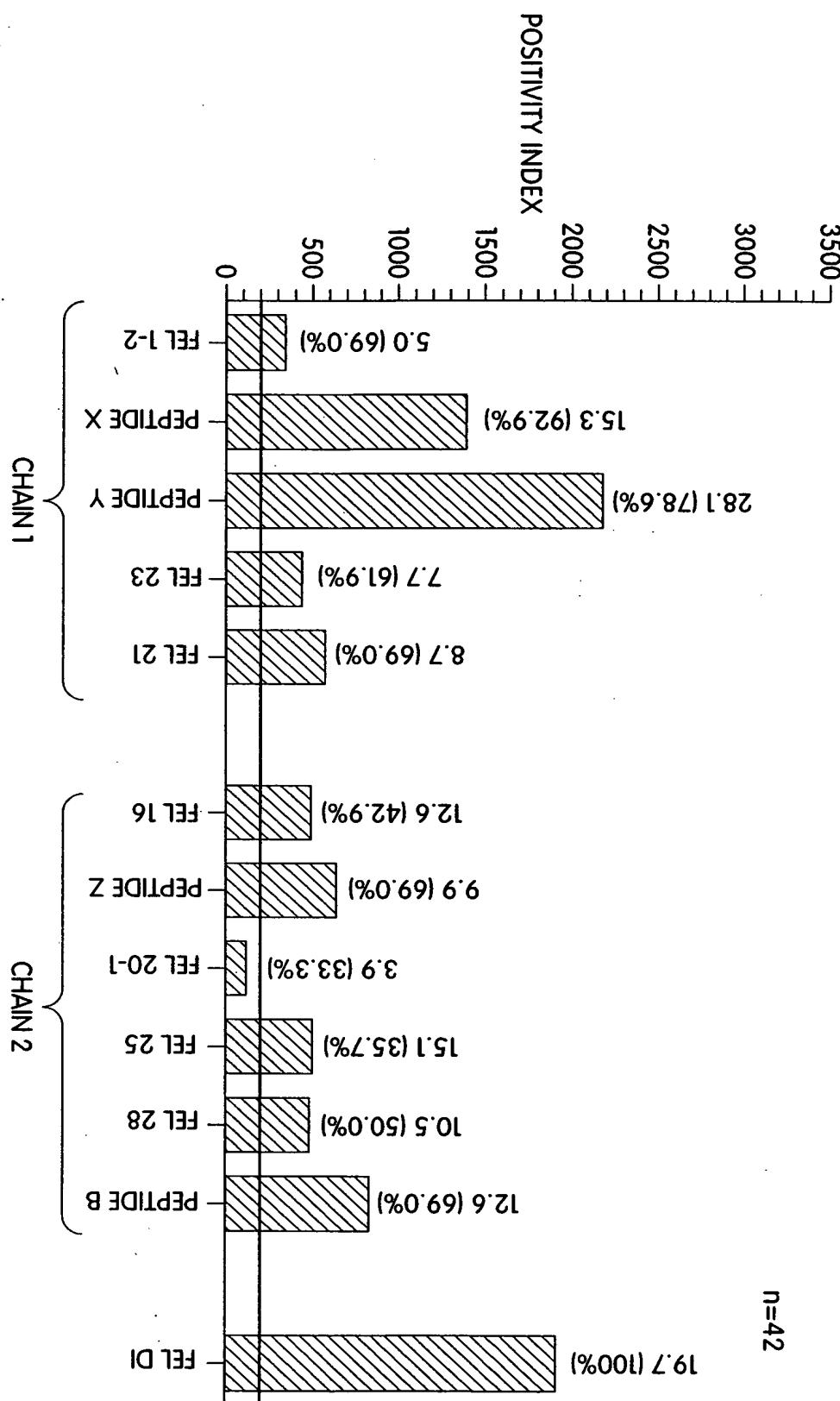


Fig. 22



Fig. 23



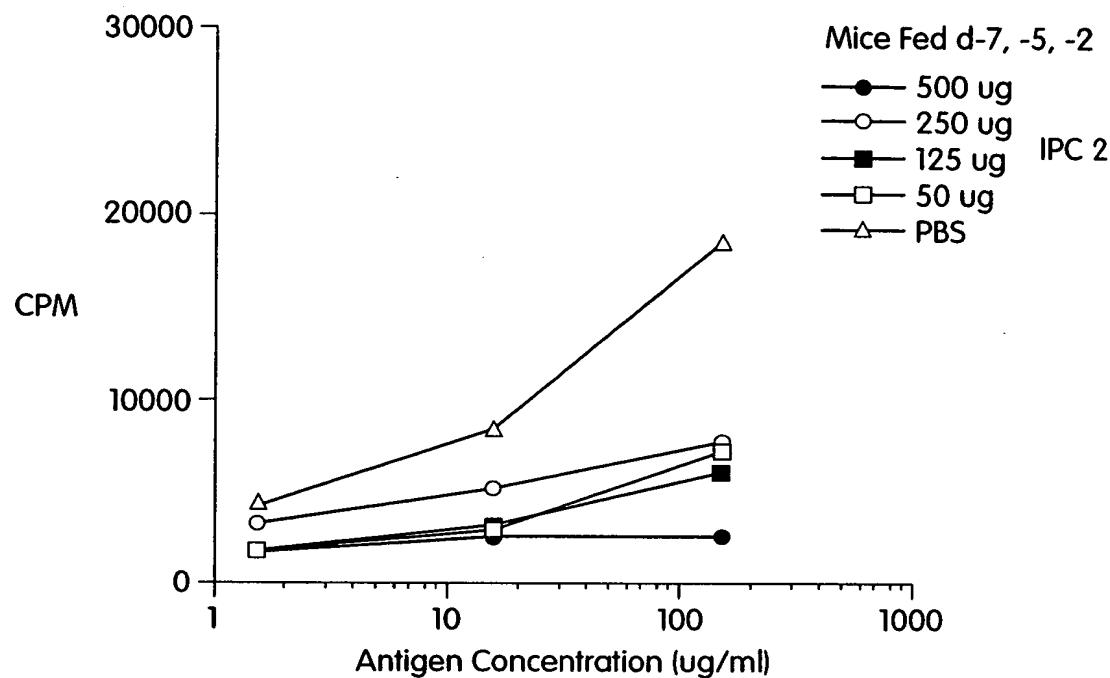


Fig. 24A

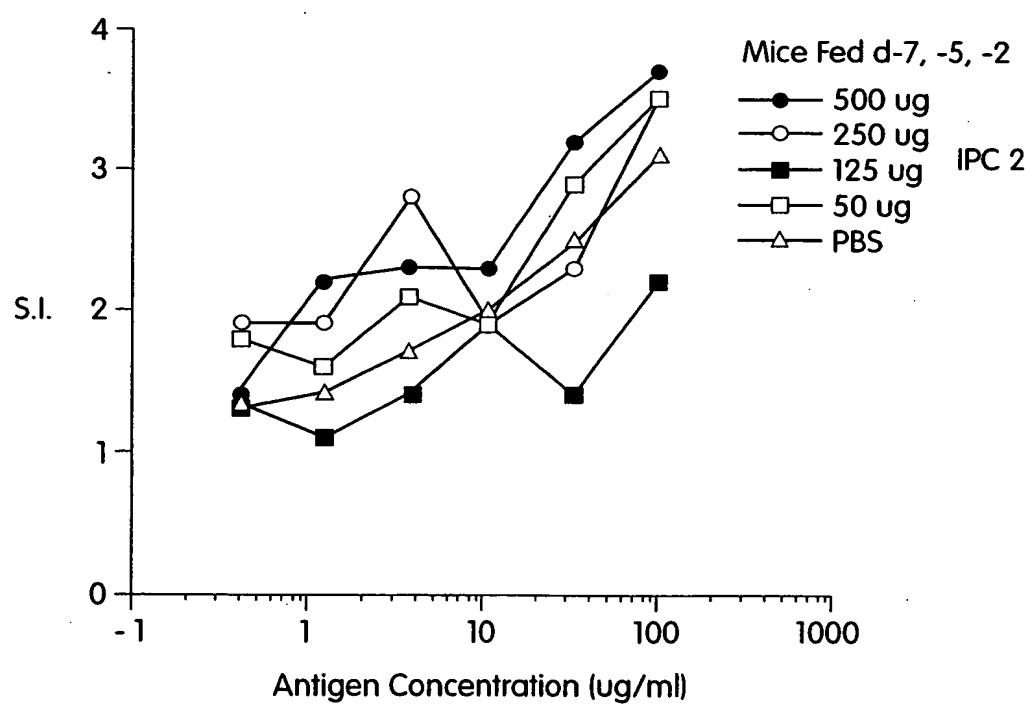


Fig. 24B

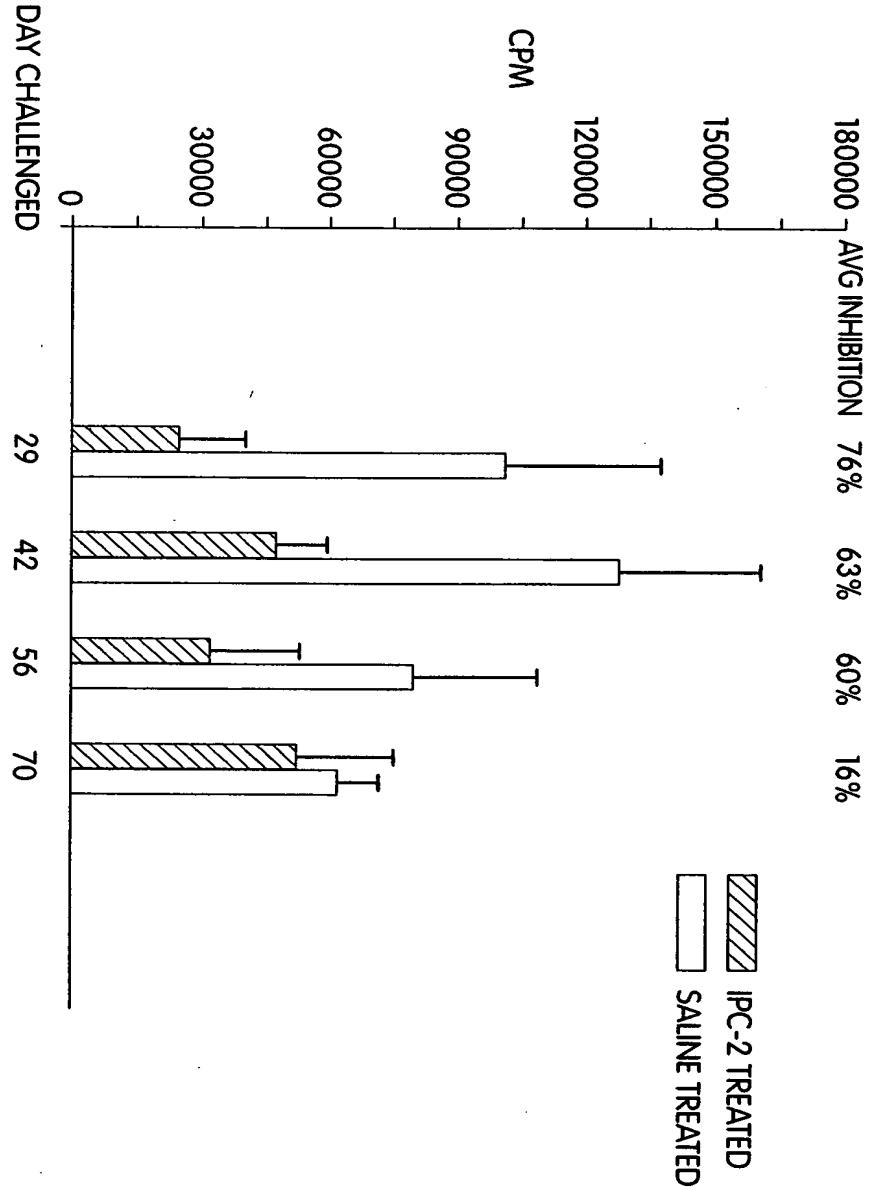


Fig. 25

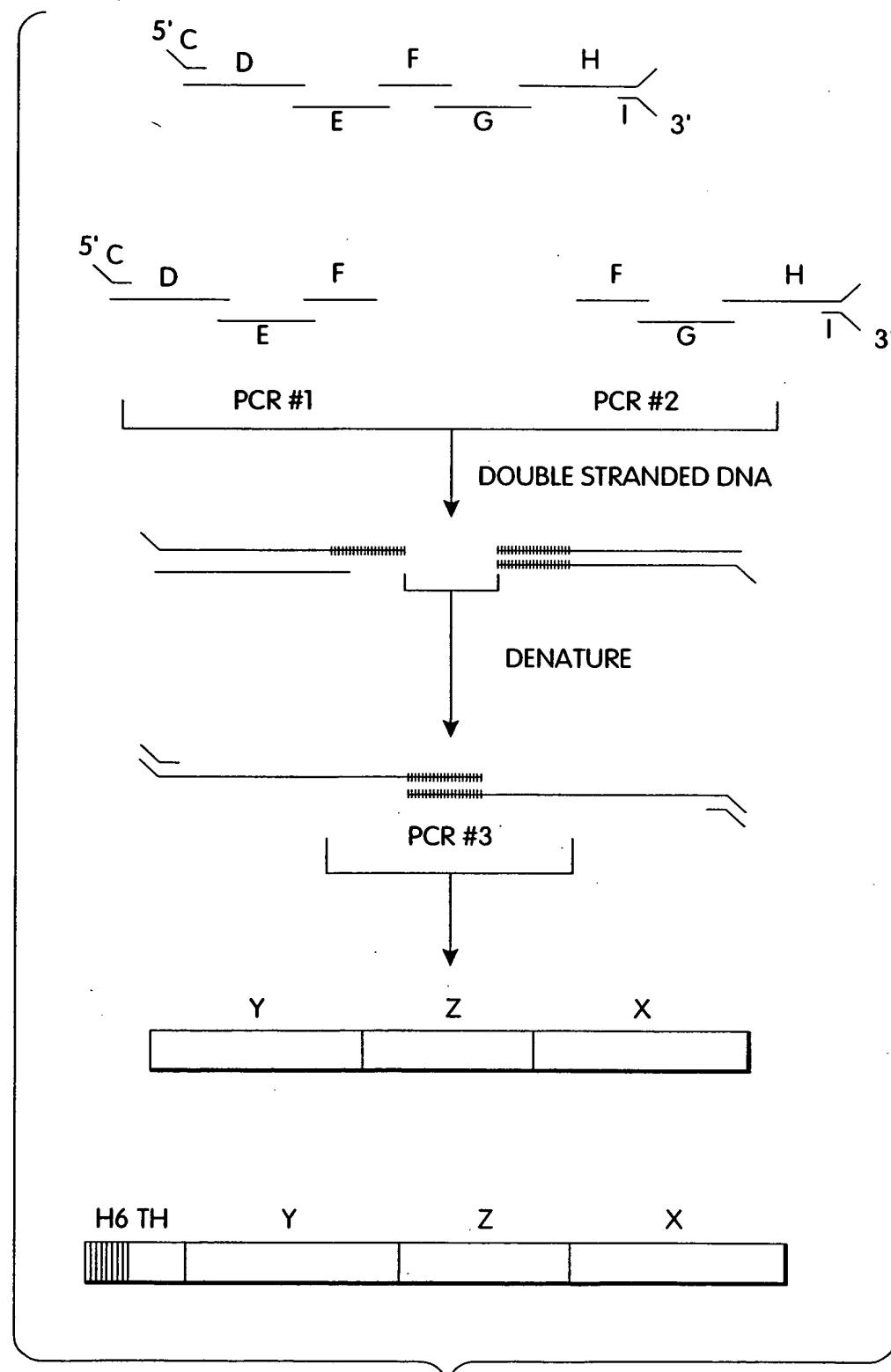


Fig. 26

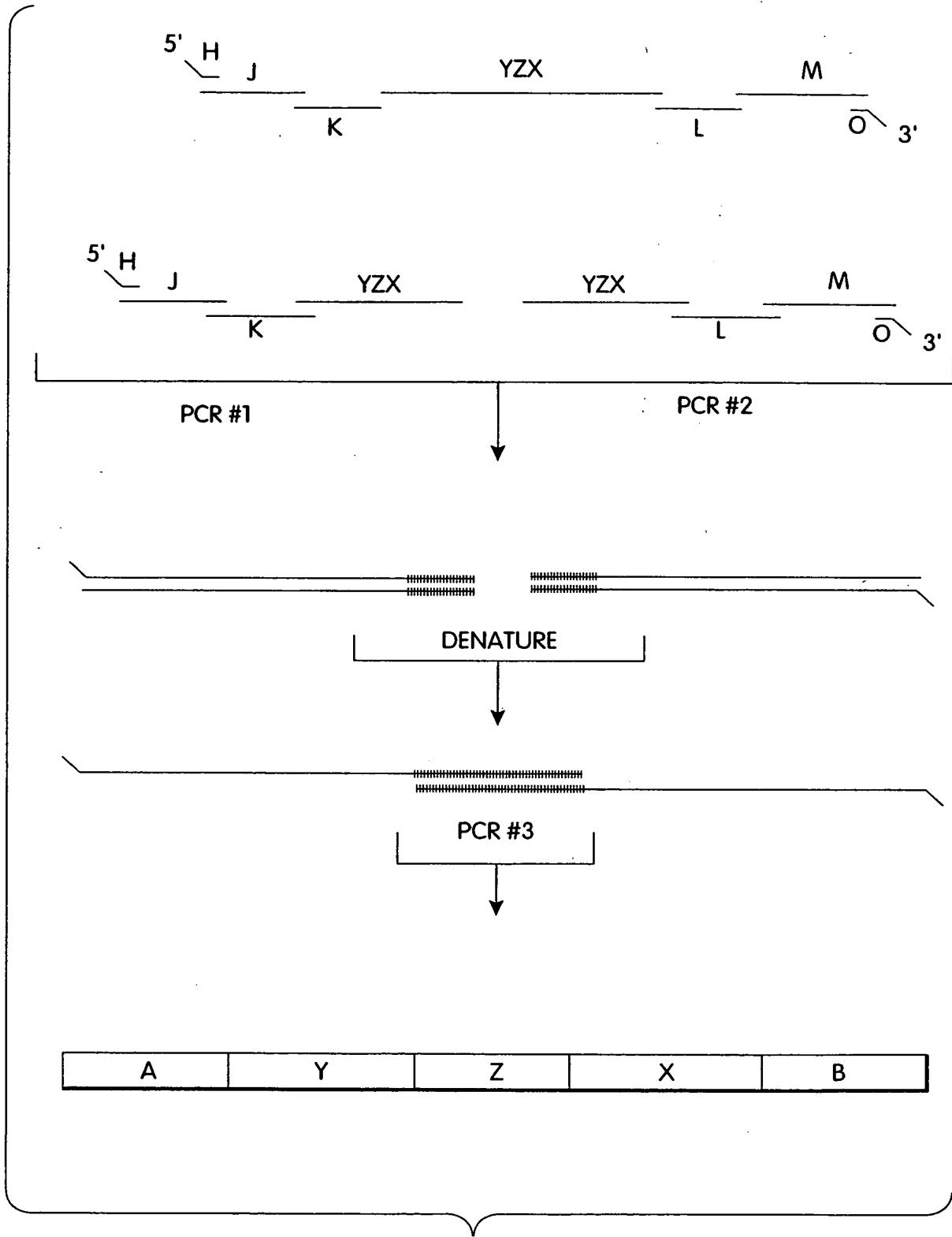


Fig. 27



C 5'      **BAM HI**  
GGGGATCCAAGCTCTGGGTT 3'  
K A L P V V

D 5'      **BAM HI**  
GGGGATCCAAGCTCTGGGTTCTGGAAAACGCTCGTATCCTGAAAGACTGCCCTGACGGCTAAATGACCGAA  
K A L P V V L E N A R I L K N C V D A K M T E  
GAAGACAAAGAA 3'  
E D K E

E 3'      CTTCTTCTGTTTCTTAAGAAAGCACAACGATTGCCATTGCTTGACGACCTGGACAGAGAC 5'  
E E D K E F F A V A N G N E L L L D L S L

F 5'      CTGGACCTGTCCTGACCAAAAGTTAACGCTAACCGAACGGAAACGT 3'  
L D L S L T K V N A T E P E R

G 3'      TGCTTGGCTTGCATTGGCAACTGGACAAAGGACTGGCCATGGGCCATGGGCCCTG 5'  
T E P E R K R D V D L F L T G T P D

H 5'      ACCGGTACCCGGACGAAATACGTTGAACAGGTTGCTCAGTACAAAGCTCTGCCGGTTAGTAGTCAGACTGGCAGAAG  
T G T P D E Y V E Q V A Q Y K A L P V - - XBAI PSTI  
CTGGGATCCCC 3'  
HINDIII ECORI

Fig. 28A



I 3' CGAGACGGCAAATCATCAGATCTGACGTCCTTGAACCTAGGG 5'  
A L P V - - XBAI PSTI HINDIII ECOLI

J 5' GGGGATCCGAGAACAAAGAAAACGGCTCTGCTGCTG 3'  
BAM HI E E D K E N A L S L L

K 3' GACAGAGACGCCTGTTAGATGTGGAGAGGGACTTCGAGACGGCCAAACAGACCTT 5'  
L S L L D K I Y T S P L K A L P V V L E

L 3' CGAGTCATGTTTCGAGACGGCCAAATACCCACTTCGACAAAGTCTTGTGGCAACTT 5'  
A Q Y K A L P V M G E A V Q N T V E

M 5' CAGAACACCGTTGAAAGACCTGAAACTGAACACCCCTGGGTGTTGAATGTAACTGCAGAATTCCCC 3'  
Q N T V E D L K L N T L G R - PSTI ECOLI

N 5' GGGGATCCGAGAACCAA 3'  
BAM HI E E D K

O 3' TGAAACCCCTCTACTTACATTGACGTCCTTAAGGGG 5'  
T L G R - PSTI ECOLI

Fig. 28B



ATGGGTCACCACCCACCAACCGAATTCTGTTCCGGGTGGATCC  
M G H H H H H E F L V P R G S

AAAGGCTCTGCCGGTTGTTCTGGAAACCGCTCGTATCCTCGTAAACGCTGC  
K A L P V V L E N A R I L K N C

GTTGACGCTAAATGACCGAAGAACAAAGAATTCTCGCTGTTGCT  
V D A K M T E E D K E F F A V A

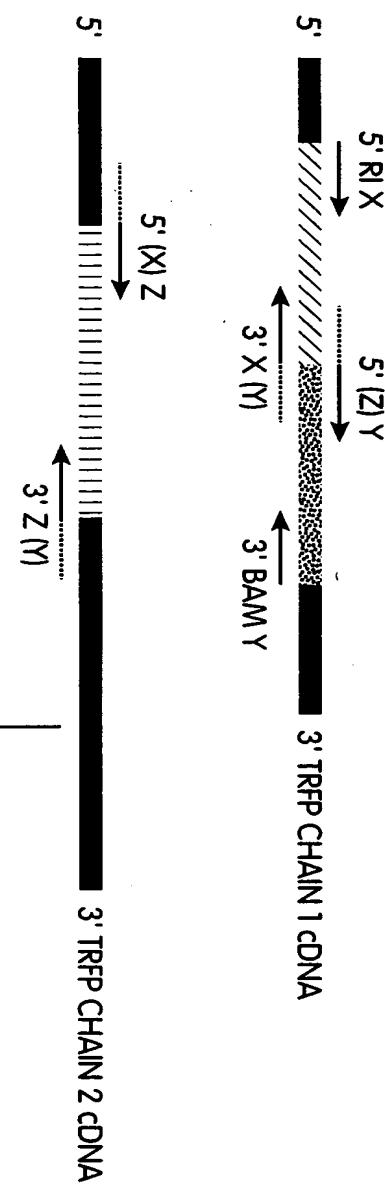
AACCGGTAACCGAACTGCTGCTGGACCTGTTCTGACCAAGTTAACGCT  
N G N E L L D L S L T K V N A

ACCGGAAACCGGAAACGGTAACCGTGCACCGTGGACCTGTTCTGACCCGGTAC  
T E P E R K R D V D L F L T G T

CCGGACCGAATACGGTTGACACGGTTGCTCACTACAAAGCTCTGCCGGT  
P D E Y V E Q V A Q Y K A L P V

Fig. 29

1) PCR INDIVIDUAL EPITOPEs



2) LINK ISOLATED EPITOPOES BY POOLING/PCR

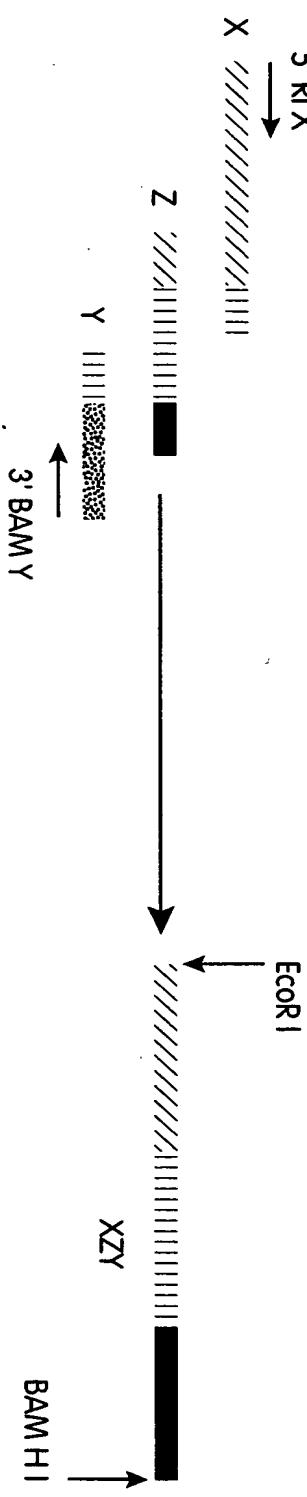


Fig. 30





### 5' PRIMERS

#### XZY CONSTRUCT

5' XRI      5' -GGGGAATTCAAGAGGGATGTTGACCTA-3'  
                   ECOR I                    X

5' (X) Z      5' -CTACCTGTATTTTTGCGGTGGCCAAT-3'  
                   X                            Z

5' (Z) Y      5' -CCAGAGAGAAAAGCACTACCTGTAGTA-3'  
                   Z                            Y

#### YXZ CONSTRUCT

5' YRI      5' -GGGGAATTCAAAGCACTACCTGTAGTA-3'  
                   ECOR I                    Y

5' (Y) X      5' -GATAAGGAGAAGAGGGATGTTGACCTA-3'  
                   Y                            X

5' (X) Z      5' -CTACCTGTATTTTTGCGGTGGCCAAT-3'  
                   X                            Z

#### ZXY CONSTRUCT

5' ZRI      5' -GGGGAATTCTTGCGGTGGCCAATGGA-3'  
                   ECOR I                    Z

5' (Z) X      5' -AAGAGGGATGTTGACCTATTC-3'  
     X

Fig. 31A



### 3' PRIMERS

#### XZY CONSTRUCT

3' X (Z) 5' - ATTGGCCACCGCAAAAAATACAGGTAGTGCTTGTA-3'  
 |  
 Z | X  
 αL αA αK | αR αE αP αE αT αA  
 3' Z (Y) 5' - TAGTGCTTTCTCTGGTTAGTAGC-3'  
 Y | Z  
 αSTOPαE αK αD αE αE αT  
 3' Y BAM 5' - GGGGATCCTTACTCCTTATCCTCTGT-3'  
 BAMH I Y

#### YXZ CONSTRUCT

3' Y (X) 5' - TAGGTCAACATCCCTCTCTCCTTATCCTCTGT-3'  
 |  
 X | Y  
 αA αF αF | αV αP αL αA αK αY  
 3' X (Z) 5' - CGCAAAAAATACAGGTAGTGCTTGTA-3'  
 Z | X  
 αSTOPαR αE αP αE αT αA  
 3' Z BAM 5' - GGGGATCCTTATCTCTGGTTAGTAGC-3'  
 BAMH I Z

#### ZXY CONSTRUCT

3' Z (X) 5' - TAGGTCAACATCCCTCTCTCCTGGTTAGTAGCATT-3'  
 |  
 X | Z  
 αSTOPαE αK αD αE αE αT αM  
 3' Y BAM 5' - GGGGATCCTCACTCCTTATCCTCTGTGTCAT-3'  
 BAMH I Y

Fig. 31B

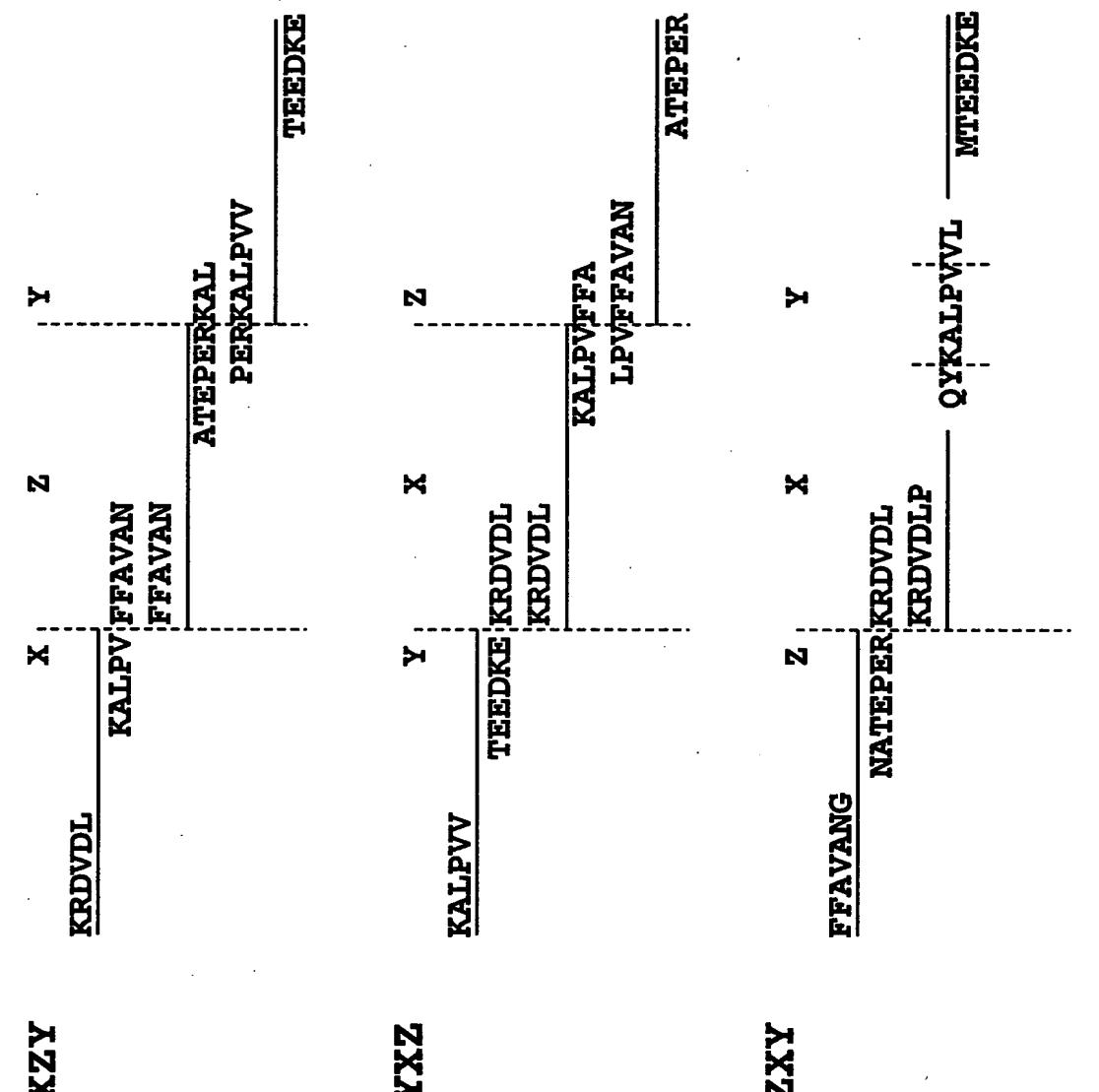


Fig. 32

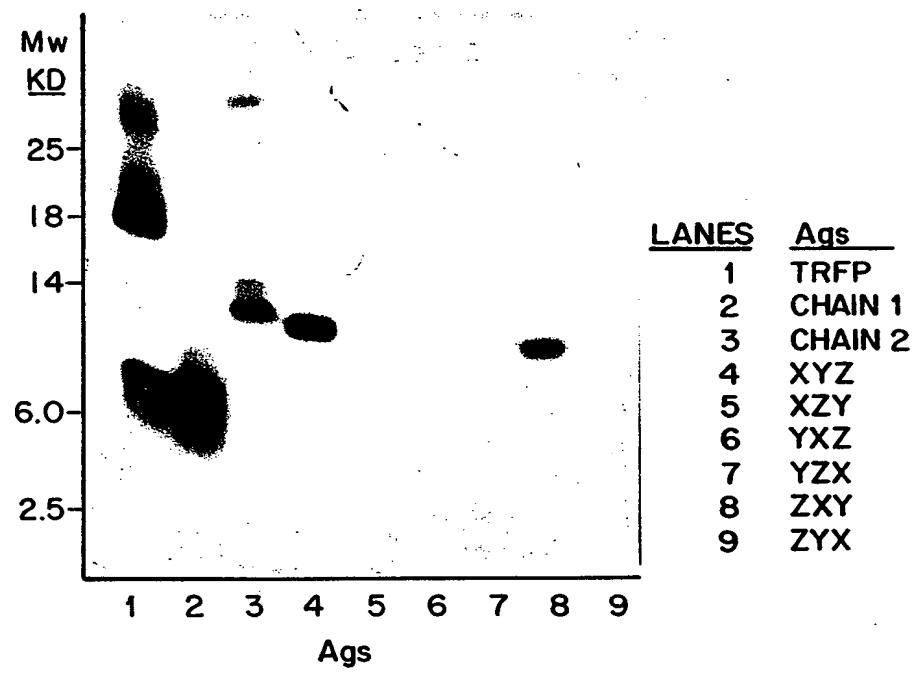
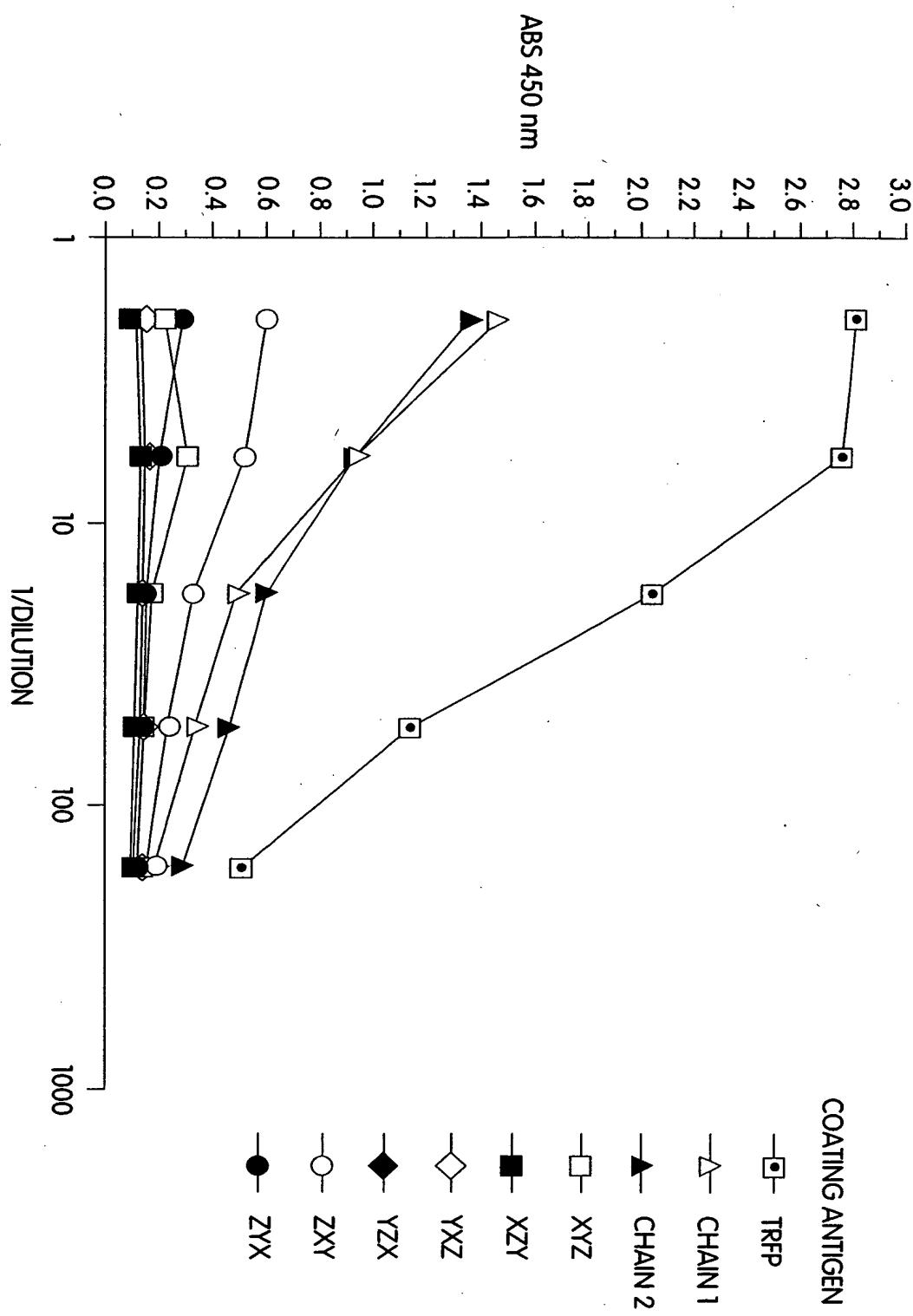


Fig. 33



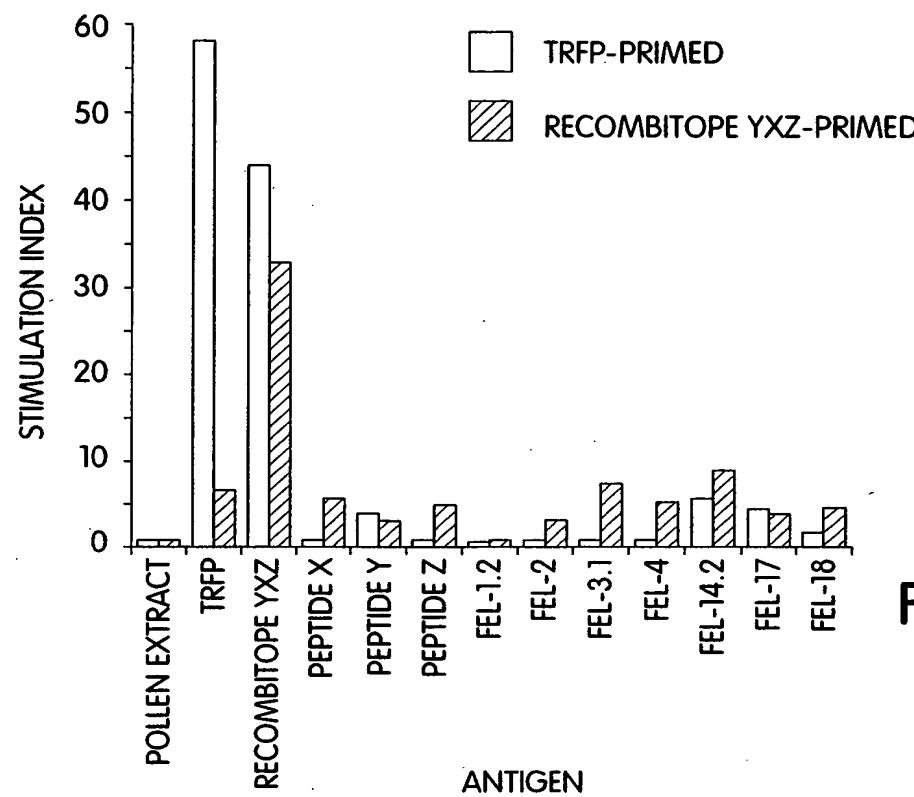


Fig. 35A

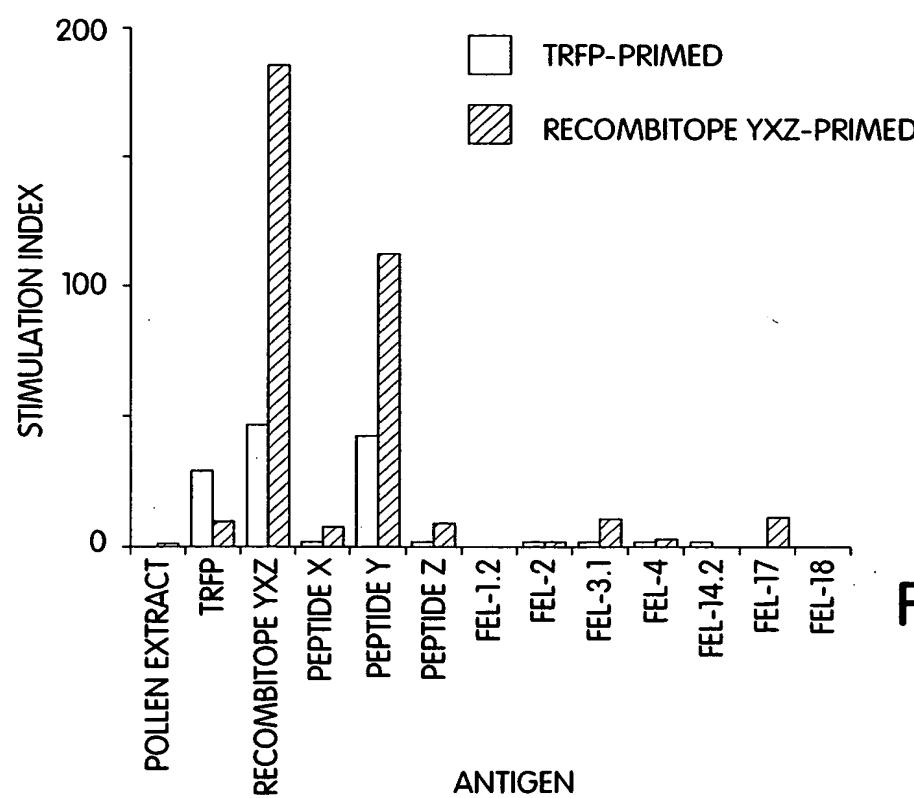


Fig. 35B

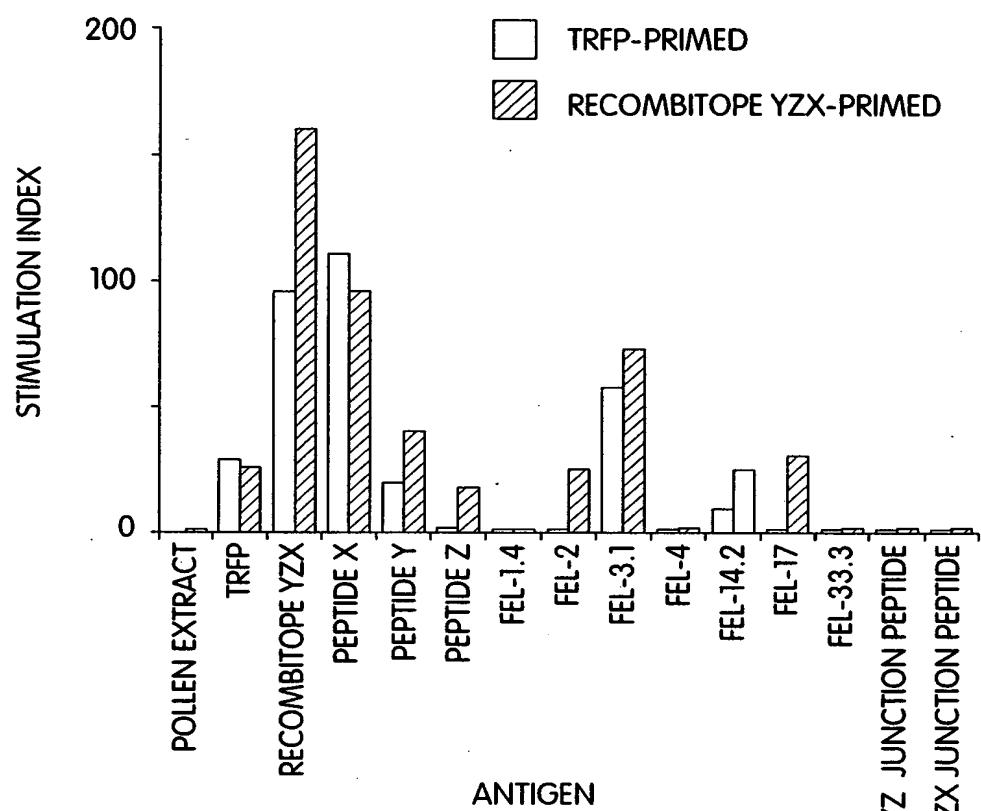


Fig. 35C

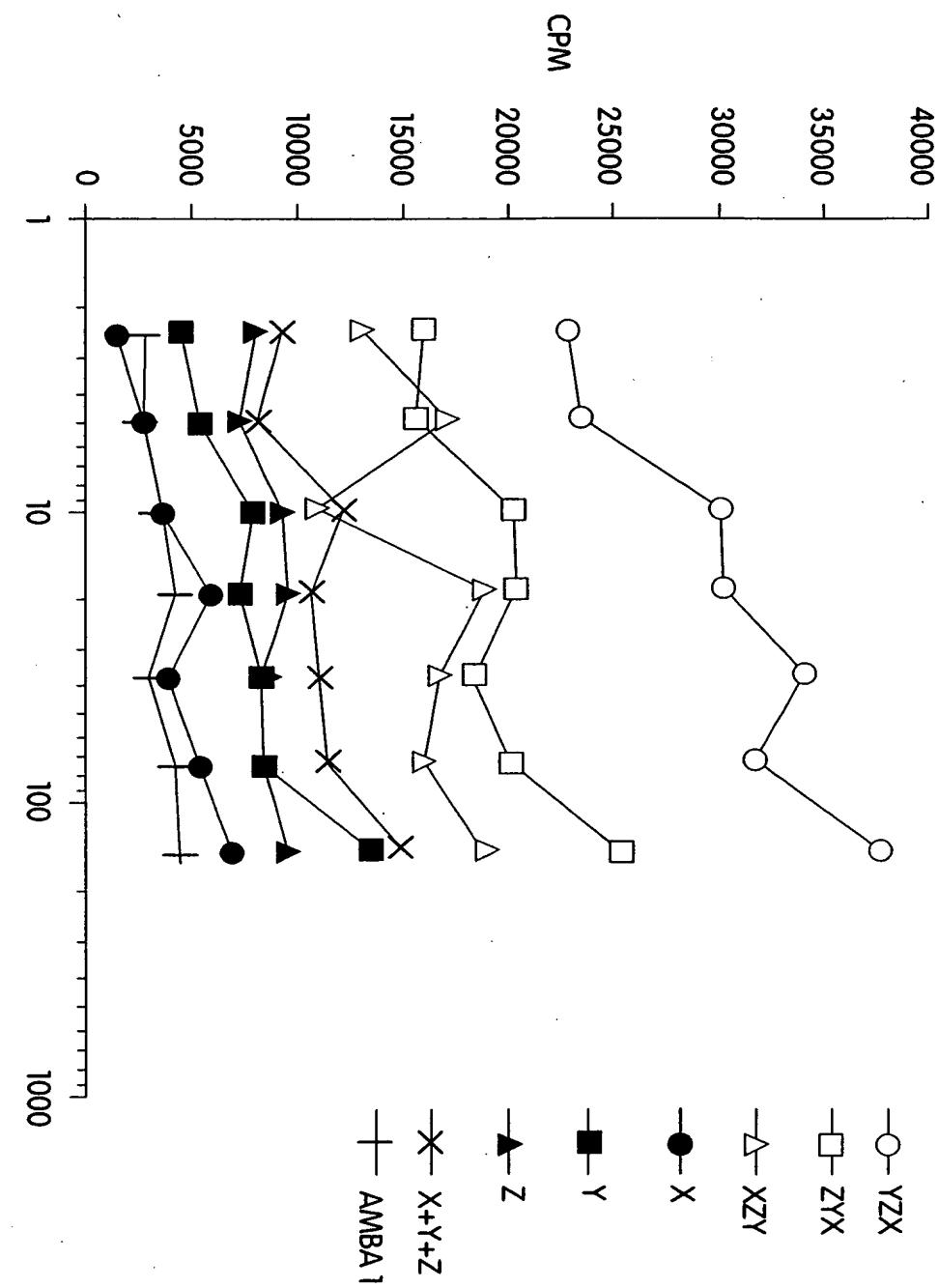


Fig. 36

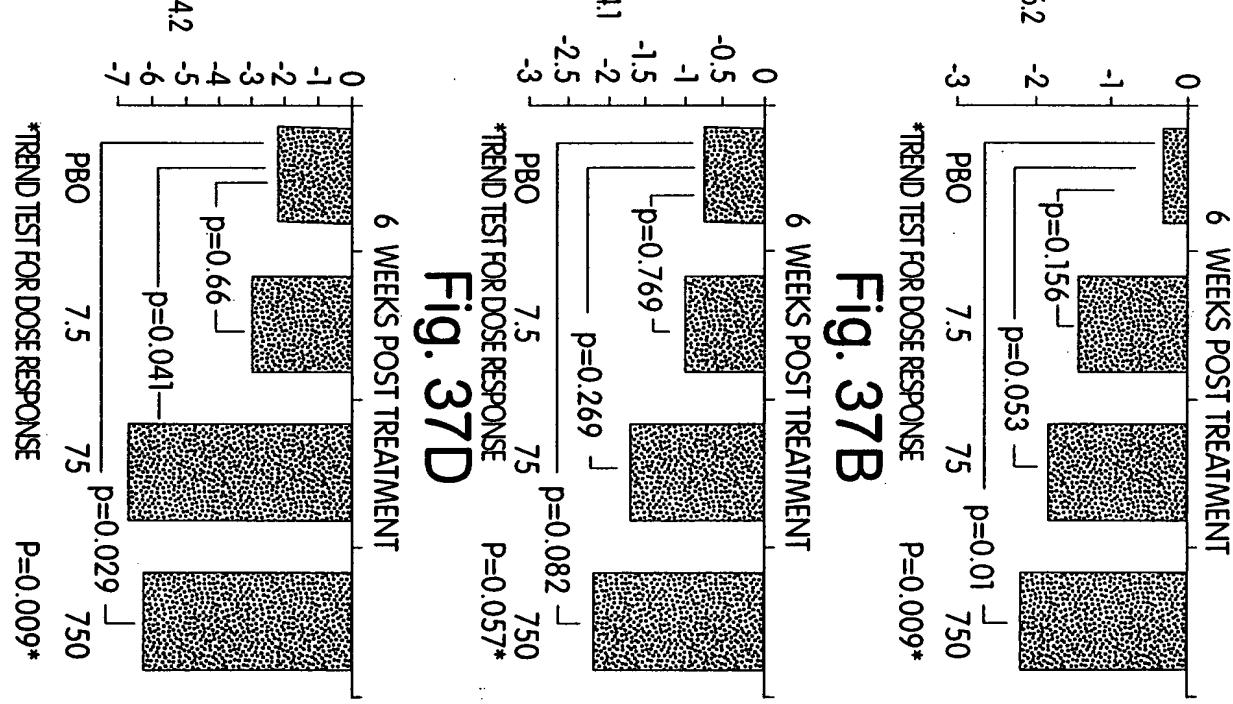
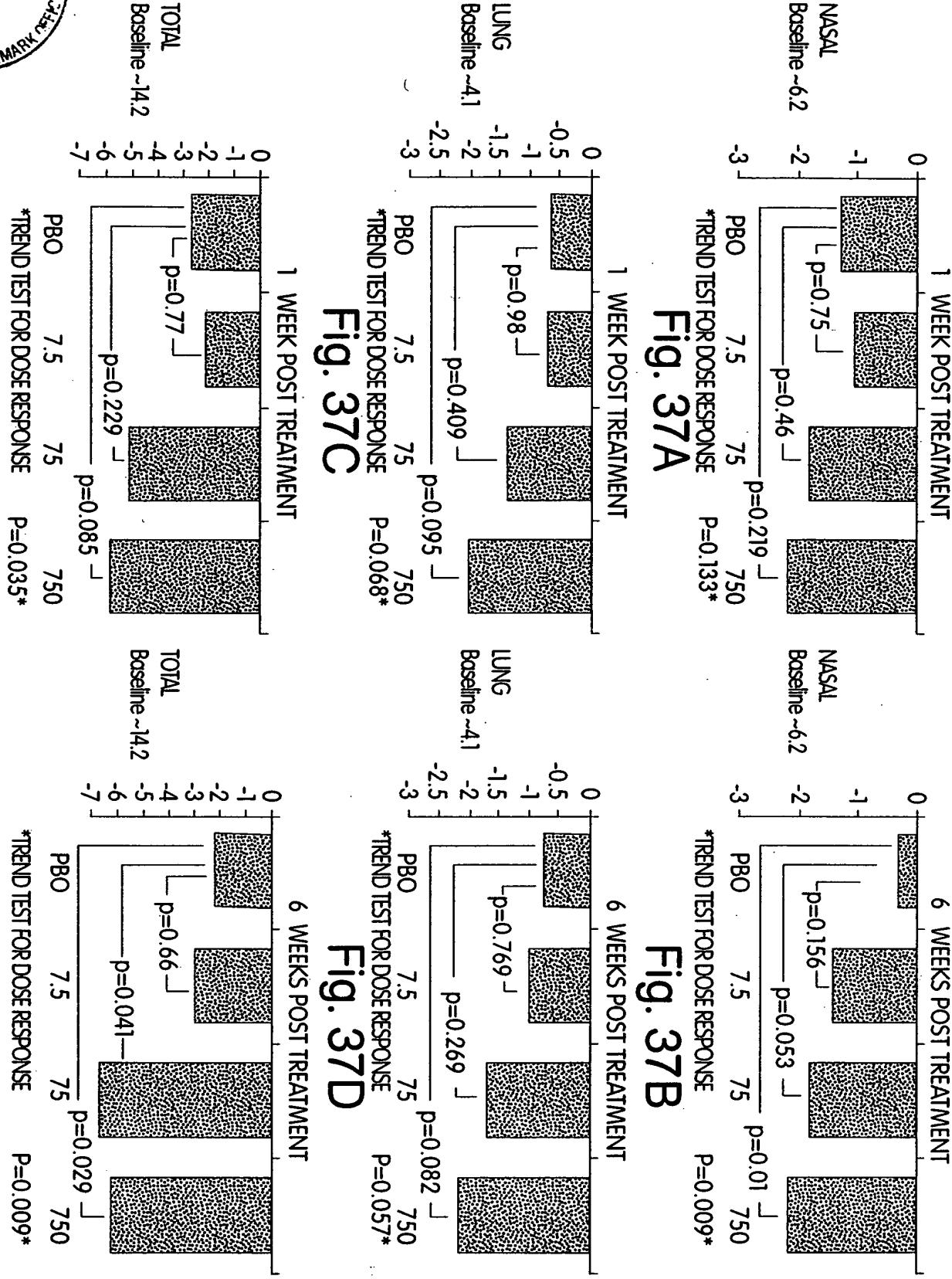
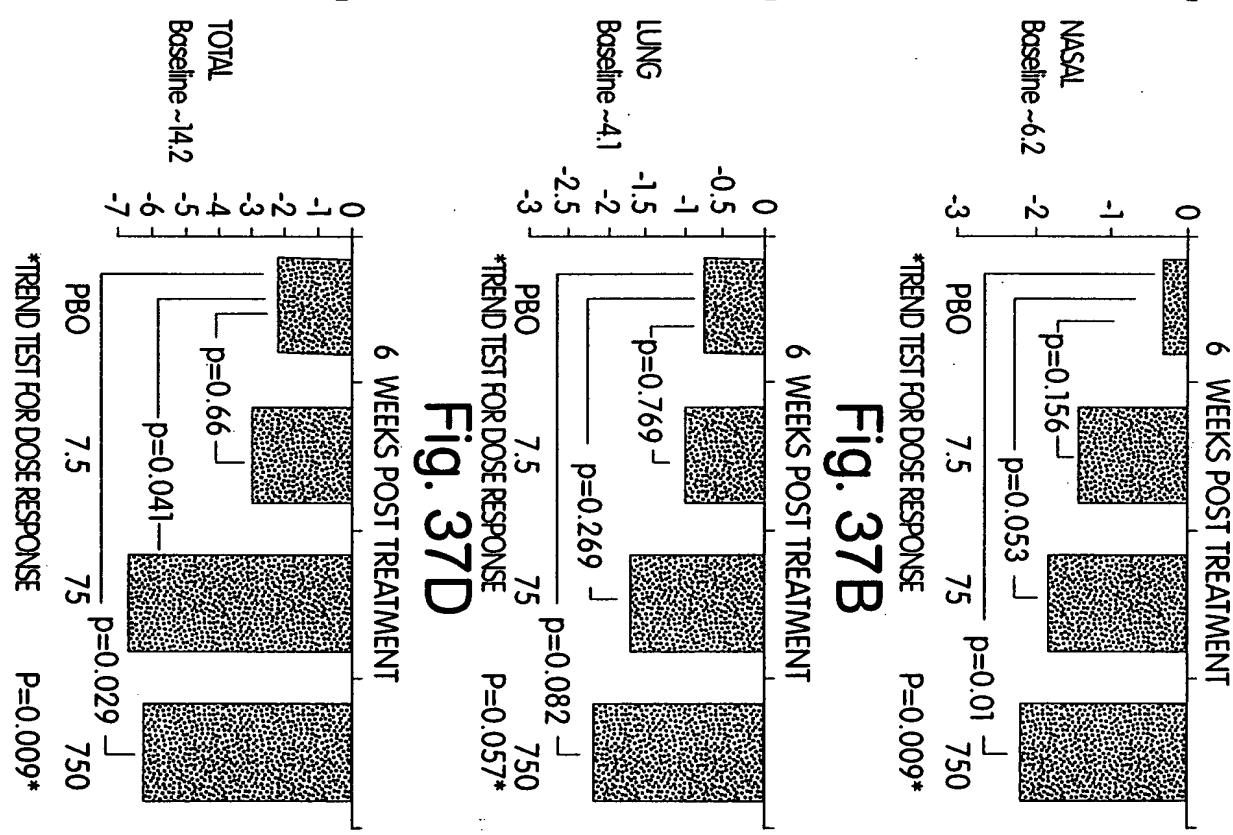
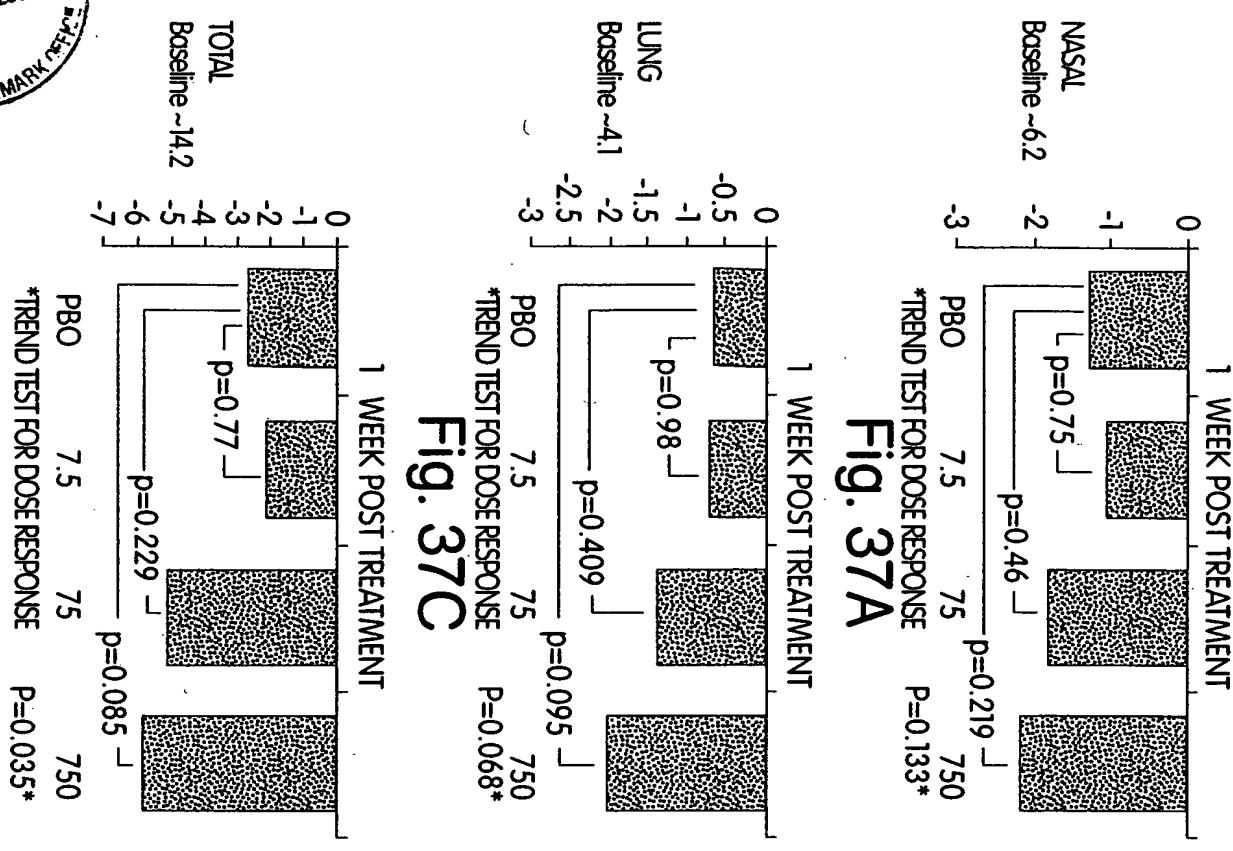


Fig. 37E

Fig. 37F